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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                      OM protein - protein search, using sw model
                                                                                                                                                        Run on:
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(without alignments) 535.879 Million cell updates/sec October 29, 2002, 03:48:42; Search time 25 Seconds

1853 1 MYNGSCCRIEGDTISQVMPP.....ANSFQSQSDGQWDPHIVEWH 346 US-09-886-041-2 Perfect score: Sequence:

105224 seqs, 38719550 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Scoring table:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0%

SwissProt\_40:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	P49019 homo sapien 000270 homo sapien 0902031 mus musculu 09ns75 homo sapien 149652 meleagris grandles and sapien 149652 meleagris grandles and sapien 149652 meleagris grandles and sapien 149650 homo sapien 149650 mus musculu 099677 homo sapien 149650 mus musculu 099677 homo sapien 141232 rattus norv 141232 rattus norv 141232 mus musculu 141232 rattus norv 141232 mus musculu 141232 mus musculu 141232 mus musculu 141231 homo sapien 14131 homo sapien 1413
SUMMARIES	HM74 HUMAN GPRV_HUMAN GFRY_HUMAN CLT2_HUMAN P27R_BUEGA P27R_BUEGA P27R_BUEGA P27R_BUEGA P27R_BUEGA P27R_HUMAN CLT2_P1G P27P_HUMAN P27S_CHICK GPRZ_HUMAN GPRZ_HUMAN GPRZ_HUMAN GPRZ_HUMAN GPRZ_HUMAN SSRZ_HUMAN SSRI_RAT CLT1_P1G SSRI_RAT CLT1_HUMAN
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Length	100 100 100 100 100 100 100 100 100 100
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% Query Match	. 440909090909088887666666666666666666666666
Score	8
Result No.	100 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0

P30680 rattus norv 063371 rattus norv P30937 mus musculu P34994 sus scrofa P31391 homo sapien 063645 rattus norv 932745 homo sapien P26824 rattus norv Q511K6 mus musculu P30936 rattus norv P55085 homo sapien
SSR2_RAT P2Y6_RAT SSR4_RAT SSR3_MOUSE SSR2_PIG SSR2_PIG SSR3_HUMAN PAR2_RAT SSR3_HUMAN THRR_RAT GPRY_MOUSE SSR3_RAT PAR2_RAT
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369 328 328 3388 3388 3483 3483 368 368 378 368 368 368 368 368 368 368 368 368 36
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300.5 300.5 300 299.5 299.5 298.5 298.5 298.5 298.5 298.5
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## ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                 Nomura H., Nielsen B.W., Matsushima K.;
"Molecular cloning of cDNAs encoding a LD78 receptor and putative leukocyte chemotactic peptide receptors.";
Int. Immunol. 5:1239-1249(1993).
-i. FUNCTION: ORPHAN RECEPTOR.
-i. SUBCELLULAR LOCATION: Integral membrane protein.
-i. SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
2 (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
5 (POTENTIAL).
6 (POTENTIAL).
6 (POTENTIAL).
6 (POTENTIAL).
7 (POTENTIAL).
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                                                                      01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Probable G protein-coupled receptor HM74.
                        387 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MIM; 606039; -.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
TISSUE-Monocytes;
MEDLINE-94092629; Pubmed-7505609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; D10923; BAA01721.1; -.
                        STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P34996; 1DDD.
GCRDb; GCR_0528; -.
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51
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                        HM74_HUMAN
P49019;
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TRANSMEM
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HM74_HUMAN
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HIDDAY
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PROSITE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                           FFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSARLYFL 244
                                                                                                                                                                                                                                MICLPFRIDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAV 124
                                                                                                                                                                          NTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIMFQLE 184
                                                                 Gaps
                                                                                     5 SCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLL 64
                                                                                                encoding a putative G protein-coupled receptor.";
Genomics 42:519-523(1997).
-I- FUNCTION: ORPHAN RECEPTOR.
-I- SUBCELLULAR LOCATION: Integral membrane protein.
-I- SUMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                              245 WTVPSSA---CD--PSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                G., Santoni A.,
                                                                 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Isolation and chromosomal localization of GPR31, a human gene
                                           Length 387;
                                                                 Indels
            C244F562C2343647 CRC64;
  CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                        300 KOPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDP 340
                                                                                                                                                                                                                                                                                                                            316 KMTGEPDNNRSTSVELTGDPNKT-RGAPEALMANSGEPWSP 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2ingoni A., Rocchi M., Storlazzi C.T., Bernardini
Napolitano M.;
                                          .5%; Score 880.5; DB 1; 2%; Pred. No. 1.1e-54; 49; Mismatches 107;
                                                                                                                                                                                                                                                                                                                                                                                                               15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Probable G protein-coupled receptor GPR31.
                                                                                                                                                                                                                                                                                                                                                                                 319 AA
                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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            BY
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PRINTS; PR00237; GPCRRHODOPSN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                       44481 MW;
                                          47.5%;
52.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U65402; AAC51375.1; -.
                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
  387
                                                                                                                                                                                                                                                                                                                                                                                                      (Rel. 36, (Rel. 36, (Rel. 40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human)
299
100
387 AA;
                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
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                                                      3est Local Sim
Matches 178;
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000270;
  DOMAIN
DISULFID
SEQUENCE
                                           Query Match
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126 LSPQAALGVSGLVWLLMVALTCPGLLISE--AAQNSTRCHSF-YSRADGSFSIIWQEALS 182
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                                                                                                                                                                                                                                                                                                                                                                                                          127 ISTRVAAGIVCTLWALVILGTVYLLLENHLCVOETAVSCESFIMESANG-----WHDIMF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                              (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 --LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKL 292
                                                                                                                                                                                                                                                                                                                                                        11;
                                                                                                                                                                                                                                                                                                                           DB 1; Length 319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        243 VLMHIFQNLGSCRALCAVAHTSDVTGSLTYLHSVVNPVVYCFSSPTFRSSYRRV
                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                        CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
                                           EXTRACELLULAR (POTENTIAL).
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                                                                                                                                       (POTENTIAL).
                                                                                                                                                                                5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
                                                                                                                                                                                                                                                              (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                         121;
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                                                                                                                                                                                                                                              7 (POTENTIAL).
CYTOPLASMIC (POT)
N-LINKED (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Cysteinyl leukotriene receptor 2 (CysLTR2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             309 AA
                                                                                                                                                                                                                                                                                                                                                         62; Mismatches
                                                                                                                        3 (POTENTIAL)
                                                             (POTENTIAL)
                                                                                                                                                                                                                                                                                                                         24.2%; Score 448.5; 34.0%; Pred. No. 1.1
toSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1. toSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1. protein coupled receptor; Transmembrane.
                                                                                                                                                     4 (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                16
37
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Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                            319 AA;
                                                                                                                                                                                                                                                                                                                                           Similarity
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PubMed=11591709;
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132
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sapiens (Human).
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EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLT2_HUMAN STANDARD; PRT; 346 AA.
09NS75; Q9HCQ2;
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Cysteinyl leukotriene receptan CysterR2) (PSEC0146) (HG57) (HPN321).
CYSLTR2 OR CYSLT2 OR CYSLT2R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59 VADFLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVV 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            119 HPHHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSC----ESFIMESA 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     174 NGWHDIMFQLEFFMPLGIILFCSFKIVWSLRRRQ--QLARQARMKKATRFIMVVAIVFIT 231
         TISSUE SPECIFICITY: Widely expressed at low levels, with highest expression in the spleen, thymus and adrenal gland, and lower in the kidney, brain and peripheral blood leukocytes. SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 YSNRNCTIE-NFKKEFYPIIYLIIFFWGALGNGFSIYVF---LQTCKKSTSVNVFMLNLA 65
                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 YNGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPST---VYLFNLA 58
                                                                                                                                                                                                                                                                                                                                                                                   LINKED (GLCNAC. . .) (POTENTIAL). 327B14A6EDDD2A02 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17;
                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CYLPSVSARLYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSF
                                                                                                                                     EMBL; AF331658; AAK97354.1; -.
EMBL; AF331658; AAK97354.1; -.
PiterPro; IPR000276; GPCR_Rhodpsn.
PFam; PF00001; 7tm.1; 1.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; FALSE_NEG.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein.
26 EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                            2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                          EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                      EXTRACELLULAR (POTENTIAL)
5 (POTENTAI)
                                                                                                                                                                                                                        1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
 SUBCELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: Widely expressed at low leve
                                                                                                                                                                                                                                                                                                                                                                                                                 20.0%; Score 371.5; DB 1; 32.7%; Pred. No. 2.5e-19; ive 56; Mismatches 125;
                                                                                                                                                                                                                                                                                                                                  (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY
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                                                                                                                                                                                                                                                                                                                                                                                              35227 MW;
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56
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171
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95
14
309 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-20459128; PubWed-10851239;
MEDLINE-20459128; PubWed-10851239;
Heise C.E., O'Dowd B.F., Figuenca D.J., Sawyer N., Nguyen T.,
Im D.-S., Stocco R., Bellefeuille J.N., Abramovitz M., Cheng R.,
Williams D.L. Jr., Zeng Z., Liu Q., Ma L., Clements M.K., Coulombe N.,
Liu Y., Austin C.P., George S.R., O'Neill G.P., Metters K.M.,
Lynch K.R., Evans J.F.;
"Characterization of the human cysteinyl leukotriene 2 receptor.";
J. Biol. Chem. 275:30531-30536(2000).
                                                                                                                                                                                                                                                                                           "The molecular characterization and tissue distribution of the human
                                                                                                                                                                                            Takasaki J., Kamohara M., Matsumoto M., Saito T., Sugimoto T., Ota T
Nishikawa T., Kawai Y., Masuho Y., Isogai T., Suzuki Y., Sugano S.,
Furuichi K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Molecular cloning and characterization of a second human cysteinyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      leukotriene receptor: discovery of a subtype selective agonist."; Mol. Pharmacol, 58:1601-1608(2000).
   Euteleostom1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nothacker H.-P., Wang Z., Zhu Y., Reinscheid R.K., Lin S.H.S.,
                           Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dunn M.; Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases
   Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                      cysteinyl leukotriene CysLT2 receptor.";
Biochem. Biophys. Res. Commun. 274:316-322(2000)
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InterPro; IPR000276; GPCR_Rhodpsn.
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   Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AB041644; BAB16379.1; -
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                                                      NCBI_TaxID-9606;
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us-09-886-041-2.std.rsp

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                                                                                                                                                                                                                                                                                                                                           PHHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSC---ESFIMESANGW 176
                                                                                                                                                                                                                                                                                                                                                                              HDIMFOLEFFWPLGIILFCSFKIVWSLRRRQ--QLARQARWKKATRFIMVVAIVFITCYL 234
                                                                                                                                                                                                                                                                                                                                                                                                                          Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosaurla; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                PSVSARLYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKI 294
                                                                                                                                                                                                                                                                                 27 NSRNCTIE-NFKREFFFPIVYLIIFFWGVLGNGLSIYVF---LQPYKKSTSVNVFMLNLAI 82
                                                                                                                                                                                                                                                     Mismatches 134; Indels 17; Gaps
                                                                                                                                                                                                                                                                     3 NGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPST---VYLFNLAV 59
                                                                                                                                                                                                                                                                                                                                                     BY SIMILARITY.

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                       (POTENTIAL).
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DEC-1998 (Rel. 37, Last annotation update)
purinoceptor 1 (ATP receptor) (P2Y1) (Purinergic receptor).
                                                                                                                                                                                                                                    DB 1; Length 346;
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; FALSE_NEG.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein.
                                                                                                 4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
                                                              2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                      EXTRACELLULAR (POTENTIAL).
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                                                                                                          5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
                                                     CYTOPLASMIC (POTENTIAL).
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Pred. No. 6.1
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MEDLINE-93285340; PubMed-8508924;
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01-FEB-1994 (Rel. 28, Last seq
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29.9%;
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                                                                                                                                                                                                                 346 AA;
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Best Local Similarity
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P34996;
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DOMAIN
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InterPro; IPR0002776; GPCR_Rhodpsn.
PROMOUL; Tru__1; Tru__1; Tru__1; Tru__1; PR00237; GPCRHODPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_FI_1; 1.
PROSITE; PS00262; G_PROTEIN_RECEP_FI_2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18 MPPLLIVAEVLGALGUGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMICLPFRTDYYLR 77
Webb T.E., Simon J., Krishek B.J., Bateson A.N., Smart T.G.,
King B.F., Burnstock G., Barnard E.A.;
"Cloning and functional expression of a brain G-protein-coupled ATP
                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
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BY SIMILARITY.
N-LINKED (GLCNAC. ..) (POTENTIAL)
N-LINKED (GLCNAC. ..) (POTENTIAL)
N-LINKED (GLCNAC. ..) (POTENTIAL)
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EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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Pred. No. 9.5e-19;
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                                                                               FEBS Lett. 324:219-225(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X73268; CAA51716.1; -.
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Best Local Similarity 29.1;
Matches 95; Conservative
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76
1115
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1177
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PDB; 1DDD; 11-JUL-96.
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362 AA;
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MEDLINE-97382456; PubMed-9240460;
MEDLINE-97382456; PubMed-9240460;
MEDLINE-97382456; PubMed-9240460;
MEDLINE-97382456; PubMed-9240460;
MEDLINE 1.0 0., Schachter J.B., Harden T.K., Nicholas R.A.;
Medlate nucleotide-promoted second messenger responses.";
MISCHAM. Blochen. Blophys. Res. Commun. 236.455-460(1997).
MISCHION: RECEPTOR FOR EXTRACELLULAR ADENIES NUCLEOTIDES SUCH AS ATT AND ADP. SEEMS TO MEDIATE ITS ACTION VIA A PERTUSSIS TOXIN INSENSITIVE G-PROTEIN, PROBABLY BELONGING TO THE GQ FAMILY THAT ACTIONATE ACTIVATE A PHOSPHATIOYLINOSITOL-CALCTUM SECOND MESSENGER SYSTEM.
MISCHALLULAR LOCATION: Integral membrane protein.

-1- TISSUE SPECIFICITY: MAINLY FOUND IN BLOOD, BRAIN, AND LUNG. TO A LESSER EXTENT IN STOMACH, GUT, AND SKELETAL MUSCLE.

-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                           138 TLWALVIL------GTVYLLLENHLCVQETA-----VSCESFIMESANGWHD 178
                                                                                                                                                                                                                                                                                                                                                                                                           Meleagris gallopavo (Common turkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Meleagrididae; Meleagris.
                                                                                                                                                                                                                                                                                                                                   01-FEB-1996 (Rel. 33, Last sequence update)
15-JUT-1998 (Rel. 36, Last annotation update)
P2X purinoceptor 1 (ATP receptor) (P2X1) (Purinergic receptor) (6H1 orphan receptor).
                                                                                                                      ----SVSARLYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNK
                          163 LVWALVVAVIAPILFYSGTGVRRNKTITCYDTTADEYLRSYFVYSMCTTVFM-----
                                                        179 IMFQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Brain;
MEDLINE=94335907; PubMed=8058061;
Filtz T.M., Li Q., Boyer J.L., Nicholas R.A., Harden T.K.;
"Expression of a cloned P2Y purinergic receptor that couples to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR00276; GPCR_Rhodpsn.
Pfam: PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein.
                                                                                                                                                                                                                                                                                        362 AA.
                                                                                                                                                                               292 LKICSLKPKQPGHSKTQRPEEMPISNL 318
                                                                                                                                                                                                           327 ATRKSSRRSEP -- NVOSKSEEMTLNIL 351
                                                                                                                                                                                                                                                                                                                   01-FEB-1996 (Rel. 33, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mol. Pharmacol. 46:8-14(1994).
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HSSP; P34996; 1DDD.
GCRDb; GCR_2392;
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                                                                                                                                                                                                                                                                                       STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                phospholipase C.";
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                                                                                                                                                                                                                                                                                    P2YR_MELGA
P49652;
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TLWALVIL------GTVYLLLENHLCVQETA------VSCESFIMESANGWHD 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78 RRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNTISTRVAAGIVC 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----SVSARLYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNK 291
                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18 MPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMICLPFRTDYYLR 77
           1 (POTENTIAL).
2 (POTENTIAL).
2 (POTENTIAL).
2 (POTENTIAL).
3 (POTENTIAL).
3 (POTENTIAL).
4 (POTENTIAL).
5 (POTENTIAL).
6 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
7 (POTENTIAL).
6 (POTENTIAL).
7 (POTENTIAL).
7 (POTENTIAL).
8 SIMILARITY.
N-LINKED (GLCNAC...) (POTENTIAL).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          179 IMFQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
TISSUE-Acrtic endothelium;
MEDLINE-95352058; PubMed-7626079;
Henderson D.J., Elliot D.G., Smith G.M., Webb T.E., Dainty I.A.;
"Cloning and characterisation of a bovine P2Y receptor.";
Blochem. Biophys. Res. Commun. 212:648-656(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
P2Y purinoceptor 1 (ATP receptor) (P2Y1) (Purinergic receptor).
                                                                                                                                                                                                                                                                                                                                                                                                19.6%; Score 364; DB 1; Length 362; 29.1%; Pred. No. 9.5e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                    58; Mismatches 130; Indels
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                              3E128AB9EB64349C CRC64;
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NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                     11
26
102
186
362 AA;
 P2YR_BOVIN
                                                  TRANSMEM
DOMAIN
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TRANSMEM
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TRANSMEM
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                RANSMEM
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337

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288 LDF-QTPEMCAFNDRVYATYQVTRGLASLNSCVDPILYFLAGDTFRRLSR----
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                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 138 TLWALVILGTVYLLLENHLCVQET-AVSC-----ESFIMESANGWHDIMFQLEFFM 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             corpus callosum.";
Neurobiol. Dis. 5:259-270(1998).
-1- FUNCTION: RECEPTOR FOR EXTRACELLULAR ADENINE NUCLEOTIDES SUCH AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18 MPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMICLPFRTDYYLR 77
                                     Deng G., Matute C., Kumar C.K., Fogarty D.J., Miledi R.; "Cloning and expression of a P2y purinoceptor from the adult bovine
                                                                                        ATP AND ADP.
-1- SUBCELLULAR LOCATION: Integral membrane protein.
-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19.6%; Score 362.5; DB 1; Length 373; 27.5%; Pred. No. 1.2e-18; tive 68; Mismatches 140; Indels 35.
                                                                                                                                                                                                                                                                                                                                                                                            3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
5 (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
6 (POTENTIAL).
7 (POTENTIAL).
                                                                                                                                                                                                                                                                                                   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                       EXTRACELLULAR (POTENTIAL).
1 (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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N-LINKED (GLCNAC. . .) (PO
9270A7175C0BDA76 CRC64;
                                                                                                                                                                                                                                                                                                                                                             CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (PC
BY SIMILARITY.
                                                                                                                                                                                                                                                                  InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
SEQUENCE FROM N.A.
TISSUE-Corpus callosum;
MEDLINE-99064562; Pubmed-9848096;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42287 MW;
                                                                                                                                                                                                                                             EMBL; U34041; AAC78275.1; -. HSSP; P34996; 1DDD.
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373 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kamohara M., Takasaki J., Matsumoto M., Matsumoto S., Saito T.,
Ohishi T., Soga T., Matsushime H., Furuichi K.;
"Characterization of the cloned rat and porcine cysteinyl leukotriene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Receptor for cysteinyl leukotrienes. The response is mediated via a G-protein that activates a phosphatidylinositol-calcium second messenger system (By similarity).
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metázoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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N-LINKED (GLCNAC. . .) (POTENTIAL).
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(GLCNAC. . .) (POTENTIAL)
(GLCNAC. . .) (POTENTIAL)
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Live 59; Mismatches 118; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          G-protein coupled receptor; Transmembrane; Glycoprotein. DOMAIN 1 43 EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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7 (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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6 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AB052662; BAB60817.1; -.
InterPro; IPR000276; GPCR_Rhodpsn.
PEdm; PF000001; 7tml; 1.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; FALSE_NEG.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 1.3e-18;
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                                                                                                                                                                                                   ...dred)
...(rel. 41, Last sequence update)
...(rel. 41, Last sequence update)
Cysteinyl leukotriene receptor 2 (CysLTR2).
Sus scrofa (PLQ).
Eukaryota: "...
QPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSD 335
                                              --ATRKASRRSEANLQSKSEDMTLNILSEFKONGD 370
                                                                                                                                                                         345 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL)
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345 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 86; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID-9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   receptors."
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TRANSMEM
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DISULFID
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PRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LFCSFKIVWSLRRRQQLARQARM -- KKATRFIMVVAIVFITCYLPSYSARLYFLWTVPSS 250
                                                                                       LRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNTISTRVAAGI 135
                                                                                                                                                                          136 VCTLWALVILGTVYLLLENHLCVQETAVSC---ESFIMESANGWHDIMFQLEFFMPLGII 192
                                                                                                                                                                                                                                                                                                         219 SICYLLIIRALLKVEVPESGLRLSHRKALITVIIALIIFLLCFLPYHVLRTLHLLEWKAD 278
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Sciurognathi; Muridae; Murinae; Rattus.
                                           99
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-1- TISSUB SPECIFICITY: EXPRESSED IN MUSCLE, HEART, LIVER, KIDNEY,
LUNG, BRAIN, SPLEEN, BUT NOT IN TESTIS.
-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                           PPLLIVAFVLGALGNGVALCGFCFHMKTWKPST---VYLFNLAVADFLLMICLPFRTDXY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POYR_RAT STANDARD; PRT; 373 AA.
P49651.
01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
P2Y purinoceptor 1 (ATP receptor) (P2Y1) (Purinergic receptor)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IFINCT.
PROMODI; TLM_1; 1.
PRINTS; PROMODI; TLM_1; 1.
PROSTTE; PROMODI; G_PROTEIN_RECEP_F1_1; 1.
PROSTTE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
PROSTTE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
PROSTTE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
PROMOTEIN_RECEP_F1_2; 1.
PROMOTEIN_
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                    251 ACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSF 285
                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U22830; AAA91303.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STORTH STATE STATE STATE STATE STATES STATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                174 LVWLIVVVAISPILFYSGTGIRKNKTVTCYDSTSDEYLRSYFIYSM-----CTTVAMFCI 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PLVLILGCYGLIVRALIYK-DLDNSPLRRKSIYLVIIVLTVFAVSYIPFHVMKTMNLRAR 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LYFLWTVPSSACD--PSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLK 298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNTISTRVAAGIVC 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TLWALVILGTVYLLLENHLCVQET-AVSC------ESFIMESANGWHDIMFQLEFFM 187
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18 MPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMICLPFRTDYYLR 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 receptors.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
-- FUNCTION: Receptor for cysteinyl leukotrienes. The response is mediated via a G-protein that activates a phosphatidylinositol-calcium second messenger system (By similarity).
--- SUBCELLULAR LOCATION: Integral membrane protein.
--- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLP----SVSAR
                                                                                                                                                                                                                                                                                                                       N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
6DDF67628785E648 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 373;
                          EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
7 (POTENTIAL).
7 (POTENTIAL).
8 SIMILARITY.
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01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Cysteinyl leukotriene receptor 2 (CysLTR2) (RSBPT32).
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19.3%; Score 358.5; DB 1; 27.0%; Pred. No. 2.3e-18; tive 68; Mismatches 139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     299 PKQPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSD 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----ATRKASRRSEANLOSKSEEMTLNILSEFKONGD 370
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hes 91; Conservative
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197
373 AA;
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167
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Q924T9;
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TRANSMEM
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59 VADFLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVV 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             119 HPHHAVNTISTRVAAGIVC-TLWALVILGTVYLLLENHLCVQETAVSCESFIMESAN--G 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               176 WHDIMFQLEFFMPLGIILFCSFKIVWSLRRRQ--QLARQARMKKATRFIMVVAIVFITCY 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 YNGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPST---VYLFNLA 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo saplens (Human).
Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                BY SIMILARITY.

N-LINKED (GLCNAC. ) (POTENTIAL).

N-LINKED (GLCNAC. ) (POTENTIAL).

N-LINKED (GLCNAC. ) (POTENTIAL).

A122AC8177879D56 CRC64;
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Rel. 95, Last sequence update)
CT-2001 (Rel. 40, Last annotation update)
purinoceptor 1 (ATP receptor) (P2X1) (Purinergic receptor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19.2%; Score 355.5; DB 1; Length 309; 31.2%; Pred. No. 3.2e-18; tive 57; Mismatches 131; Indels 13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        234 LPSVSARLYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSF 285
                                                                     EMBL; AB052661; BAB60816.1; -.
Interpreted: PR000276; GPCR_Rhodpsn.
Pfam; PF000017; Tum_1; 1.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; FALSE_NEG.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein.
26 EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                              4 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

6 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                  6 (POTENTIAL).

EXTRACELULAR (POTENTIAL).

7 (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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Matches 91; Conservative
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272. 293
293. 3
95. 1
14. 166. 1
167. 1
309 AA;
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SEQUENCE FROM N.A.
TISSUE-Placenta;
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1120
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1188
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P47900;
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CARBOHYD
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The first partial forms of the first part of the following statement of the
                                                                                                                                                                                                                                                                                                                                                                                                   Ayyanathan K., Tania W., Harbansjit S., Raghbir A.S., Barnard E.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
PRNINS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G_POTEIN_RECEP_Fl_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_Fl_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Platelet;
MEDLINE-96257237; PubMed-8666290;
Leon C., Vial C., Cazenave J.-P., Gachet C.;
"Cloning and sequencing of a human cDNA encoding endothelial P2Y1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Janssens R., Communi D., Pirotton S., Samson M., Parmentier M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Cloning and tissue distribution of the human P2X1 receptor."; slochem. Blophys. Res. Commun. 221:588-593(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 95-373 FROM N.A., FUNCTION, AND INHIBITION STUDIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Leon C., Vial C., Weber J., Cazenave J.-P., Gacher C., Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Cloning and chromosomal localization of the human P2Y1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Blochem. Biophys. Res. Commun. 218:783-788(1996).
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                                                                                                                                                       purinoceptor.";
Gene 171:295-297(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kunapuli S.P.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biochem.
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HSSP;
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                                                                                                     EMBL; U22829; AAA91302.1; -.
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147
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197
373 AA;
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ches 91; Conserv
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TRANSMEM
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CARBOHYD
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TOKUYAMA Y., Hara M., Jones E.M.C., Fan Z., Bell G.I.;
TOKUYAMA Y., Hara M., Jones E.M.C., Fan Z., Bell G.I.;
"Cloning of rat and mouse P2Y purinoceptors.";
Blochem. Biophys. Res. Commun. 211:211-218(1995).
-I. FUNCTION: RECEPTOR FOR EXTRACELLULAR ADENINE NUCLEOTIDES SUCH AS ATP AND ADP. IN PANCREATIC ISLETS, MAY MEDIATE SOME OF THE EFFECTS OF EXTRACELLULAR ATP ON INSULIN SECRETION.
                                                                                                                                                                                                                                                                           PLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLP-----SVSAR 240
                                                                                                                                                                                                                                                                                                                                                   RRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNTISTRVAAGIVC 137
                                                                                                                                                                                                                                                                                                      TLWALVILGTVYLLLENHLCVQET-AVSC------ESFIMESANGWHDIMFQLEFFM 187
                                                                                                                                                                                                                                                                                                                                                                            LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK 300
                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                               MPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMICLPFRTDYYLR 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                     N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
                                                                                                                              N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                               28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
P2Y purinoceptor 1 (ATP receptor) (P2Y1) (Purinergic receptor).
                                                                                                                                                                                            DB 1; Length 373; 4.8e-18;
                                                                                                                                                                                                             66; Mismatches 132; Indels
                                                                                           EXTRACELLULAR (POTENTIAL).
                   EXTRACELLULAR (POTENTIAL)
                                             4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                          4DC7C668B4145392 CRC64;
                                                                         CYTOPLASMIC (POTENTIAL).
                                                                                                   7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
  CYTOPLASMIC (POTENTIAL).
                                      CYTOPLASMIC (POTENTIAL).
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                                                                5 (POTENTIAL).
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                                                                                                                                                                   MISSING (IN
                                                                                                                                                                                           19.1%; Score 354; 29.2%; Pred. No. 4
                                                                                                                                                                                                      Pred. No.
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                                                                                                                                                                          42071 MW;
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                                                                                                                                                                                                             Conservative
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87
1009
1126
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1166
1188
2218
2233
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2303
3328
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333
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75
88
110
1127
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167
186
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339
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les 93; Conserv
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P49650;
 DOMAIN
TRANSMEM
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TRANSMEM
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CARBOHYD
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                             PRANSMEM
                                                      DOMAIN
                                                                                           DOMAIN
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                    DOMAIN
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P2YR_MOUSE
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Matches
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      174 LVWLIVVVAISPILFYSGTGTRKNKTVTCYD---TTSNDYLRSYFIYSMCTTVAMFCIPL 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNTISTRVAAGIVC 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FLWTVPSSACD - - PSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK 300
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    I- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

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2 (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
4 (POTENTIAL).
4 (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                             GCRDb; GCR_1703; -.
MGD; MGI:105049; P2ryl.
MGD:MGI:105049; P2ryl.
InterPro: IPRO00275; GPCR_Rhodpsn.
PFRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein couple receptor; Transmembrane; Glycoprotein.
DOMAIN.
1 52 EXTRACELLULAR (POTENTAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LINKED (GLCNAC. . .) (PC 944125E9F4560BB3 CRC64;
SUBCELLULAR LOCATION: Integral membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 7.2e-18;
; Mismatches 143;
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DOMAIN
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P2Y5_CHICK
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                                                                                                                                                                                                                                                                                                                                                                                                                   HIPPOCAMPUS.
                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-97366605; PubMed-9223435;
Janssens R., Boeynaems J.M., Godart M., Communi D.;
"Cloning of a human heptahelical receptor closely related to the P2Y5
                                                                      9) (G protein-coupled
                                                                                                                                                                                                                                                                                                                                                                                          -i- SUBCELLULAR LOCATION: Integral membrane protein.
-i- TISSUE SPECIFICITY: NOT DETECTED IN THE BRAIN REGIONS THALAMUS, PUTAMEN, CAUDATE, FRONTAL CORPEX, PONS, HYPOTHALAMUS, HIPPOCAMPI-
-i- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                    Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                           O'Dowd B.F., Nguyen T., Jung B.P., Marchese A., Cheng R., Heng H.H.Q., Kolakowski L.F. Jr., Lynch K.R., George S.R.; "Cloning and chromosomal mapping of four putative novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE: PS50263; G_PROTEIN_RECEP_F1_2; 1.
G_protein coupled receptor; Transmembrane; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

Bohm S.K., Khitin L.M., Payan D.P., Bunnett N.W.;
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                Biochem. Biophys. Res. Commun. 236:106-112(1997)
       P2Y9_HUMAN STANDARD; PRT; 370 AA.
Q99677; 015132;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
P2Y purinoceptor 9 (P2Y9) (Purinergic receptor
Cepetor GPR23) (P2Y5-11ke receptor).
                                                                                                                                                                                                                               G-protein-coupled receptor genes.";
Gene 187:75-81(1997).
                                                                                                                                                                                 MEDLINE-97225799; PubMed-9073069;
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EMBL; U90323; AAB62087.1; -.
EMBL; U90322; AAB6208.1; -.
EMBL; AF005419; AAB66322.1; -.
HSSP; P34996; 1DDD.
GCRDb; GCR_1323; -.
GCRDb; GCR_1324; -.
GCRDb; GCR_1324; -.
GCRDb; GCR_1324; -.
MIM; 300086; -.
                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Primates;
                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                             NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                         48 VVFILGLITNSVSLEVECFRMKMRSETAIFITNLAVSDLLEVCTLPFKI-FYNFNRHWPF 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                GDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNTISTRVAAGIVCT-LWAL 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----DPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPK-FYNKLKICSLKPKQPGHSK 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   143 VILGTVYLLLENHLCVQETAVSC-ESFIMESANGWHDIMFQLE------FFMPLGIILF 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kaplan M.H., Smith D.I., Sundick R.S.; "Identification of a G protein coupled receptor induced in activated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T cells.";
J. Immunol. 151:628-636(1993).

- Immunol. 151:628-636(1993).

- SUBCELLULAR LOCATION: Integral membrane protein.

- SUBCELLULAR LOCATION: INDUCED IN ACTIVATED T-CELLS.

- TISSUE SPECIFICITY: INDUCED IN ACTIVATED T-CELLS.

- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                             VAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMICLPFRTDYYLRRHWAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         166 VLSGGISASLFSTTNVNNATTTCFEGF --- SKRVWKTYLSKITIFIEVVGFIIPLILNVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                195 CSFKIVWSLRRRQQLAR-QARMKKATRFIMVVAIVFITCYLPSVSARLYFLWTVPSSAC-
                                              N-LINKED (GLCNAC. . .) (POTENTIAL).
F -> L (IN REF. 3).
20857F52A3929E48 CRC64;
                                                                                                                                                                                                                                     18.7%; Score 346.5; DB 1; Length 370; 31.2%; Pred. No. 1.6e-17; Live 52; Mismatches 128; Indels 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-0CT-1993 (Rel. 27, Created)
01-0CT-1993 (Rel. 27, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
P2Y purinoceptor 5 (P2Y5) (Purinergic receptor 5) (6H1).
CYTOPLASMIC (POTENTIAL).
                           SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-93329058; PubMed-8393036;
                                                                                                                                                                                    41895 MW;
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370 AA;
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P32250;
                                                                                                                                                                                                                                                                                            95;
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CONFLICT
SEQUENCE
                           DISULFID
CARBOHYD
                                                                               CARBOHYD
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                      Pfam; PF00001; 7tm_1; 1.

PRINTS; PR01067; P2YSPRNCCPTR.

PRINTS; PR01157; P2PURNOCEPTR.

PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

G_Protein coupled receptor; Transmembrane; Glycoprotein; Lipoprotein;
                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDILEP-96145150; Pubmed-8558062;
Raport C.J., Schweickart V.L., Chantry D., Eddy R.L. Jr., Shows T.B.,
Godiska R., Gray P.W.;
                                                                                                                                                                                                                                                                                                                                                                                    GDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNTISTRVAAGIVC-TLWAL 142
                                                                                                                                                                                                                                                                                                                                          143 VILGTV---YLLLENHLCVQETAVSCESFIMESANGWHDIMFQL------EFFMPLGII 192
                                                                                                                                                                                                                                                                                                                                                          141 VLAGSTPASFFQSTNRQNNTEQRICFENF --- PESTWKTYLSRIVIFIEIVGFFIPLILN 197
                                                                                                                                                                                                                                                                                                                                                                          LFCSFKIVWSLRRRQQLAR-QARMKKATRFIMVVAIVFITCYLP-SVSARLYFLW---TV 247
                                                                                                                                                                                                                                                                                                                                                                                                          PSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPKQPGHSKT 307
                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                            24 VAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMICLPFRTDYYLRRHWAF 83
                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                       (POTENTIAL).
                                                                                                                                                                                                                                              Length 308;
                                                                                                                                    18.3%; Score 339; DB 1; Length 30 30.3%; Pred. No. 4.5e-17; Live 56; Mismatches 123; Indels
                                                                                      1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                               EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                             4214E969633B6F7D CRC64;
                                                                                                                      3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Putative G protein-coupled receptor GPR17 (R12).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 339 AA
                                                                                                                                                                                                                       POTENTIAL
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       scrob; GCR_0689; -.
InterPro; IPR000276; GPCR_Rhodpsn.
                                                                                                                                                                                                                             35597 MW;
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                                                                                                                                                                                                                      86
308 AA;
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Q13304;
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                                                                                          TISSUE-Hippocampus;
MEDLINE-98181695; PubMed-9523551;
Blaesius R.H., Weber R.G., Lichter P., Ogilvie A.;
Blaesius R.H., Weber R.G., Lichter P., Ogilvie A.;
A novel orphan G protein-coupled receptor primarily expressed in the brain is localized on human chromosomal band 2q21.";
J. Neurochem. 70:1357-1365(1998)
I. FUNCTION: ORPHAN RECEPTOR. POTENTIAL CHEMOKINE RECEPTOR.
I- SUBCELLUIAR LOCATION: Integral membrane protein.
I- SIBCLERIY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67 CLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNT 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          127 ISTR--VAAGIVCT-LWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIMFQL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            184 EFFMPLGIILFCSFKIVWSLRRRQQLARQARMK-KATRFIMVVAIVFITCYLP-SVSARL 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGQETPLENMLFASFYLLDFILALVGNTLALMLFIRDHKSGTPANVFLMHLAVADLSCVL 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EXTRACELLULAR (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

CYPOLASMIC (POTENTIAL).

4 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

5 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

6 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

7 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

8Y SIMILARITY.

N-LINKED (GLCNAC. ..) (POTENTIAL).

N-LINKED (GLCNAC. ..) (POTENTIAL).

N-LINKED (GLCNAC. ..) (POTENTIAL).

N-LINKED (GLCNAC. ..) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54; Mismatches 153; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BD2AEDB2FEBF15E1 CRC64;
w members of the chemokine receptor gene family.";
Leukoc. Biol. 59:18-23(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000276; GPCR_Rhodpsn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37826 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; 033447; AAB16746.1; -. EMBL; 294154; CAB08107.1; -. HSSP; P34996; 1DDD. GCRD; GCRL 1968; -. GCRD; GCR_2597; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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176
176
339 AA;
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                                                                     SEQUENCE FROM N.A.
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169
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299 PKQPGHSKTQRPEEMPIS 316 | | | | | | 317 LKGPPPSFEGKTNESSLS 334

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Search completed: October 29, 2002, 04:52:57 Job time: 27 secs

us-09-886-041-2.std.rpr

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
```

OM protein - protein search, using sw model

October 29, 2002, 04:51:26; Search time 44 Seconds (without alignments) 755.612 Million cell updates/sec Run on:

US-09-886-041-2 1853 1 MYNGSCCRIEGDTISQVMPP......ANSFOSOSOGQWDPHIVEWH 346 Title: Perfect score:

Scoring table: Sequence:

283138 seqs, 96089334 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

283138 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR\_71:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	DB ID	2 I69202 G protein-coupled	S33733 G	JC4162 P2	JC4737	JC5549 he	I50241	ut	A47556 ATP recept	151667	157940	C41795 somatostatin	A41795 somatostatin				JQ1488	148705	A45291		I55450	A47249	2 A44021	2 JC2083 somatostatin	2 JN0605 somatostatin	2 A46226	2 A43448	11 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
	Query Match Length	387	362	373	373	370	308	344	373	420	363	391	391	391	359	369	364	399	369	369	328	384	428	369	388	418	432	•
æ	Query	47.5	19.6	19.6	19.1	18.5	18.3	17.5	17.3	16.8	16.7	16.6	16.5	16.5	16.4	16.3	16.3	16.3	16.2	16.2	16.2	16.2	16.2	16.2	16.1	16.1	16.1	
	Score	880.5	364	362.5	354	343.5	339	324	320	310.5	309.5	307	305.5	305.5	304.5	302.5	302	302	300.5	300.5	300	300	300	299.5	299	298.5	298.5	000
	Result No.		7	e	4	ഗ	ø	7	œ	σ	10	11	12	13	14	15	16	17	18	19	50	21	22	23	24	25	56	7

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δ g RESULT 2 S33733 G protein-coupled receptor - chicken C;Species: Gallus gallus (chicken)

angiotensin II rec P-20 nucleotide re somatostatin recep delta opioid recep G protein-coupled G protein-coupled G protein-coupled angiotensin II rec delta opioid recep angiotensin II rec chemokine (C-C) re delta opioid recep G protein-coupled probable chemoattr angiotensin II rec	IENTS		
A48857 JC4629 138532 138532 105553 JC5653 JC2134 S44425 S44425 S44425 JC2134 A45177 A45177 A45177 JC677	ALIGNMENTS	RESULT 1 169202 G protein-coupled receptor HM74 - human C; Species: Homo sapiens (man) C; Date: 12-Aug 1996 #sequence_revision 12-Aug-1996 C; Accession: 169202 Int. Immunol. 5, 1239-1249, 1993 A; Title: Molecular cloning of cDNAs encoding a LD7. A; Tate ference number: 154751; MUID: 94092629 A; Are ference number: 154751; MUID: 94092629 A; Coros-references: GB: D10923; NID: 9219866; PIDN: BA; Coros-references: GB: D10923; NID: 9219866; PIDN: BB; Coros-references: GB: D10923; NID: 9219866; PIDN: B1D1	TVHLLKKKLI
000000000000000		HM74 an) nce_re .; bag; of cD ; MUID nslate 023; N 00pled 7.5%; ive .; ive	VGL
33 347 347 347 347 347 347 347 347 347 3		l receptor HM74 - sapiens (man) sapiens (man) 129-1249, mats. 1239-1249, 1993 nr cloning of cDN rr: 154751; MUID: nary; translated mRNA " < RES> s: GB:D10923; NI protein-coupled protein-coupled protein-sapies s: GB:D10923; NI protein-coupled protein-coupled protein-coupled fill:	LLWGIT
0.000000000000000000000000000000000000		uupled receptions sapiens uug-1996 #seq 169202 .; Neelsen, B .; 5, 1239-12 .; 6cular clonil number: 1547 169202 eliminary: t. 169202 rendes: 6B:D rences: 6B:D re	TAALIS
296 296 296 297 297 297 298 288 288 288 288 288 288 288 288 288		RESULT 1 169202 G protein-coupled receptor HM74 C;Species: Homo sapiens (man) C;Date: 12-Aug-1996 #sequence_L R;Nomura, H; Nielsen, B.W.; Ma A;Title: Molecular cloning of c A;Reference number: 154751; MU1 A;Accession: 169202 A;Residues: 1-387 <res a;cross-references:="" a;gene:="" c;gene:="" c;superfamily:="" c;superfamily<="" g="" gb:d10923;="" hm74="" protein-couple="" td=""><td>137 NKISNW</td></res>	137 NKISNW
04044067800444440		RESULT 1 169202 G protein-co C; Species: H C; Date: 12-A C; Accession: R; Nomura, H. Int. Immunol A; Title: Mol A; Reference C; Genetics: A; Genetic	Db 1:

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288
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                                                           T.G.; King, B.F.; Burnstoc
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                                                                                                    A,Title: Cloning and functional expression of a brain G-protein-coupled ATP receptor. A,Reference number: $33733; MUID:93285340
A,Recession: $33733
A,Status: preliminary
A,Molecule Lype: mRNA
A,Residues: 1-362 <WEB>
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C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 24-Sep-1999 C;Accession: S3373;
C;Accession: S3373;
F;Webb, T.E.; Simon, J.; Krishek, B.J.; Bateson, A.N.; Smart, T.G.; King, B. FEBS Lett. 324, 219-225, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Species: Bos primigenius taurus (cattle)
Date: 12-Oct-1995 #sequence_revision 10-Nov-1995 #text_change 24-Sep-1999
                                                                                                                                                                                                                                          A;Residues: 1-362 <WEB>
A;Residues: 1-362 <WEB>
A;Cross-references: EMBL:X73268; NID:g395084; PIDN:CAA51716.1; PID:g395085
C;Superfamily: ATP receptor P2u
C;Keywords: G protein-coupled receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TLWALVIL------GTVYLLLENHLCVQETA------VSCESFIMESANGWHD 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            163 LVWALVVAVIAPILFYSGTGVRRNKTITCYDTTADEYLRSYFVYSMCTTVFM----- 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                179 IMFQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLP--- 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   215 -----FCIPFIVILGCYGLIVKALIYK-DLDNSPLRRKSIYLVIIVLTVFAVSYLPFHV 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNTISTRVAAGIVC 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     236 ----SVSARLYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNK 291
                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18 MPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMICLPFRTDYYLR 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transmembrane protein
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C.Date: 12-Oct-1995 #sequence_revision lu-mov.....
C.Accession: JC4162
R.Henderson, D.J.; Elliot, D.G.; Smith, G.M.; Webb, T.E.; Dainty, I.A.
B.Jochem. Blophys. Res. Commun. 212, 648-656, 1995
A.Title: Clonding and characterisation of a bovine P2Y receptor.
A.Reference number: JC4162; MUID:95352058
A;Accession: JC4162
A;Accession: JC4162
                                                                                                                                                                                                                                                                                                                                                                       19.6%; Score 364; DB 2; Length 362; 29.1%; Pred. No. 4.6e-26; Live 58; Mismatches 130; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       General bovp2y

C. Superfamily: ATP receptor P2u
C. Seywords: glycoprotein; phosphoprotein; receptor; transme
F; 52-77/Domain: transmembrane #status predicted <TM1>
F; 124-150/Domain: transmembrane #status predicted <TM4>
F; 171-191/Domain: transmembrane #status predicted <TM4>
F; 214-237/Domain: transmembrane #status predicted <TM5>
F; 51-282/Domain: transmembrane #status predicted <TM5>
F; 305-328/Domain: transmembrane #status predicted <TM5>
F; 11, 27, 113, 197/Pinding site: carbohydrate (Asn) (covalent)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          292 LKICSLKPKQPGHSKTQRPEEMPISNL 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             327 ATRKSSRRSEP--NVQSKSEEMTLNIL 351
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Matches 95; Conserv
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                                                                                                                                                                                                                                                                                                                                                                             Query Match
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Length 373;

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UC414.7 Species - House receptor P271 - human

W.Alternate names: P271 purinergic receptor; P271 purinoceptor
C.Species: Howo sapiens (man)
A.Fresidues: 1-373 cJAN
A.Fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A)Gene P271; GDB:P2RV1
A)Cross-references: GDB:677125; OMIN:601167
A)Cross-references: GDB:677125; OMIN:601167
C)Superfamily: APP receptor P2u
C)Superfamily: Transmembrane #status predicted <TM3>
F)121-191/Domain: transmembrane #status predicted <TM4>
F)214-237/Domain: transmembrane #status predicted <TM5>
                                           ;
                                                                                                                                                                                                                                                                                                                                                                                188 PLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLP-----SVSAR 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78 RRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNTISTRVAAGIVC 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        138 TLWALVILGTVYLLLENHLCVQET-AVSC-----ESFIMESANGWHDIMFQLEFFM 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK 300
                                               Gaps
                                                                                                                                      18 MPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMICLPFRTDYYLR 77
                                               Indels
                                               Mismatches 140;
    Pred. No. 6.6e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPGHSKTORPEEMPISNLGRRSCISVANSFQSQSD 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -- ATRKASRRSEANLOSKSEDMTLNILSEFKONGD 370
                                           68;
27.5%;
    Best Local Similarity 27.5
Matches 92; Conservative
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cells

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in activated T
                                                                                                                                                                                                                                                     N.Alternate names: purinoceptor 6H1.
C.Species: Gallus gallus (chicken)
R.R.Kaplan, M.H.; Smith, D.I.; Sundick, R.S.
J. Immunol. 151, 628-636, 1993
A.Fitle: Identification of a G protein coupled receptor induced in activated
A.Reference number: 150241; MUID:93329058
         : | | |
RMESLFKT 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84 GDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNTISTRVAAGIVC-TLWAL 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  143 VILGTV---YLLLENHLCVQETAVSCESFIMESANGWHDIMFQL------EFFMPLGII 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-308 cKAP->
A;Cross-references: GB-L06109; NID:9304383; PIDN:AAB06587.1; PID:9304384
B;Webb, T.E.; Kaplan, M.G.; Barnard, E.A.
Biochem Biophys: Res. Commun. 219, 105-110, 1996
A;Title: Identification of 6H1 as a P2Y purinoceptor: P2Y5.
A;Reference number: JC4618; MUID:96190677
A;Accession: JC4618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PID:9304384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 308;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:L06109; NID:g304383; PIDN:AAB06587.1; A;Experimental source: T-cells C;Comment: This receptor plays a role in T-cell activation.
         C;Keywords: G protein-coupled receptor; transmembrane pr
F;15-40/Domain: transmembrane #status predicted cTM1>
F;51-74/Domain: transmembrane #status predicted cTM2>
F;89-109/Domain: transmembrane #status predicted cTM3>
F;133-153/Domain: transmembrane #status predicted cTM4>
F;177-201/Domain: transmembrane #status predicted cTM4>
F;277-248/Domain: transmembrane #status predicted cTM5>
F;269-292/Domain: transmembrane #status predicted cTM5>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56; Mismatches 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18.3%; Score 339; DB 2;
Llarity 30.3%; Pred. No. 8.1e-24;
Conservative 56; Mismatches 123;
                                                                                                                                                                                                                                           - chicken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: p2Y5
C;Superfamily: ATP receptor P2u
                                                                                                                                                                                                                                           protein-coupled receptor
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
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                                                                          308 QRP 310
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                                                                                                                          337
                               282
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F;261-282/Domain: transmembrane *status predicted <TM6>
F;305-328/Domain: transmembrane *status predicted <TM7>
F;11,27,113,197/Binding site: carbohydrate (Asn) (covalent) *status predicted
F;258,336/Binding site: phosphate (Ser) (covalent) (by protein kinase A) *status predict
F;330,339/Binding site: phosphate (Thr) (covalent) (by protein kinase C) *status predict
F;343/Binding site: phosphate (Ser) (covalent) (by protein kinase C and calmodulin-depen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Homo sapiens (man)
C;Date: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 24-Sep-1999
C;Date: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 24-Sep-1999
C;Date: 02-Sep-1997 #sequence_revision 05-Sep-1999
R;Janssens, R.; Boeynaems, J.M.; Godart, M.; Communi, D.
Biochem. Blophys. Res. Commun. 236, 106-112, 1997
A;Title: Cloning of a human heptahelical receptor closely related to the P2Y5 receptor. A;Reference number: JC5549; MUID:97366605
A;Accession: JC5549
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A;Residues: 1-370 <3NA.
A;Cross-references: DDBJ:AF005419; NID:g2240034; PIDN:AAB66322.1; PID:g2240035
C;Superfamily: ATP receptor P2u
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                                                                                                                                                                                                                                                                                       TLWALVILGTVYLLLENHLCVQET-AVSC------ESFIMESANGWHDIMFQLEFFM 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       174 LVWLIVVVAISPILFYSGTGVRKNKTITCYDTTSDEYLRSYFIYSM-----CTTVAMFCV 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48 VVFILGLITUSVSLFVFCFRMKRRSETAIFITULAVSDLLFVCTLPFKI-FYNFNRHWPF 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84 GDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNTISTRVAAGIVCT-LWAL 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  143 VILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIMFQLE-----FFMPLGIILFC 195
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                                                                                                                                                                                                                                                                                                                                                        RRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNTISTRVAAGIVC 137
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                                                                                                                                                                                                                                                            18 MPPLLIVAFVLGALGNGVALCGFCFHMKTWRPSTVYLFNLAVADFLLMICLPFRTDYYLR 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    166 VLSGGISASLFSTTNVNNATTTC--FEGLSKRVWKTYLSKITIFIEVVGFIIPLILNVSC
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                                                                                                                                                                   19.1%; Score 354; DB 2; Length 373; 29.2%; Pred. No. 4e-25;
                                                                                                                                                                                                                 66; Mismatches 132; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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Pred. No. 3.8e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QPGHSKTQ-RPEEMPISNL 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RRSEANLOSKSEDMTLNIL 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 18.5%;
1 Similarity 31.0%;
94; Conservative 5
                                                                                                                                                                                      Local Similarity 29.2
nes 93; Conservative
                                                                                                                                                                   Query Match
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Matches
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NyAlternate names: sometorion release-inhibiting factor subtype 28 receptor
NyAlternate names: sometorions (Norway rat)
C;Decise: Rattus norvegicus (Norway rat)
C;Dete: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 24-Nov-1999
C;Accession: 157940; 157949; 539244
R;O'Carroll, A.M.; Loleit, S.J.; Konig, M.; Mahan, L.C.
Mol. Pharmacol. 42, 939,946, 1992
A;Title: Molecular cloning and expression of a pituitary somatostatin receptor with processions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J.; Ishii, M.; Ishii, K.; Nanevicz, T.; Turck, C.W.; Vu,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       thrombin receptor - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
R;Gerszten, R:E: Chen, J: Ishii, M.; Ishii, K:; Nanevicz, T.; Turck, C.W.;
Nature 368, 648-651, 1994
A;Title: Thrombin receptor's specificity for agonist peptide is determined by Reference number: IS1667; MUID: 94195429
A;Accession: IS1667
A;Status: preliminary; branslated from GB/EMBL/DDBJ
A;Rolecule type: mRNA
A;Residues: 1-420 <GER>
                                                                                                    LRWGRARYARRVAANVWVLVLACQAPVLYFVTTSVRGTRITCHDTSARELFSHFVAYSS- 200
                                                                                                                                                                                                                   :| | | : | | : | | | | | : | | | : | | | : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
                                                                                                                                                                                                                                                                                                                                                        ---FIMESAN 174
                                                                                                                                                                        GIILFCSFKIVWSLRRRQQ-----LARQARMKKATRFIMVVA 226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----YL 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :U09632; NID:9495197; PIDN:AAA18498.1; PID:9495198
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                                                                                                                                                                                                                                                                                                                LYFLWTVPSSACDP--SVHGALHITLSFTYMNSMLDPLVYYFSSP
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                                       LWALVILGTVYLLLENHLCVQETAVSCES-
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PPTEPTPSPQAR 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                         VPKQPGHSKTQR 309
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Matches 88; Conservative
                                   VNTISTRVAAGIVÇ
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219 YMACSFIWLISIAS
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|160 YHLSGNDWLFGPGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   134 GIVCT-LWALVILĞ
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                 N.Alternate names: G-protein coupled receptor (S.Species: Homo sapiens (man) (S.Species: Homo sapiens (S.Species: Homo sapiens (S.Species: Trumpp, A.; Khitin, L.M.; Kong, W.; Payan, D.G.; Bunnett, N.W. Submitted to the BMBL bata Library, April 1997
A.Research (S.Species: 126705
A.Research (S.Species: Library, April 1997
A.Research (S.Species: Lanslated from GB/EMBL/DDBJ
A.Molecule type: mRNA
A.Molecule type: mRNA
A.Molecule type: mRNA
A.Residues: 1-344 <BOH>
A.Cross references: EMBL:AF000546; NID:92232068; PID:92232069
C.Genetics: (S.Seperiamily: ATP receptor P2u
C.Superfamily: ATP receptor P2u
C.Superfamily: ATP receptor; transmembrane protein
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C:Species: Mus musculus (house mouse)
C:Species: Mus musculus (house mouse)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-Sep-1999
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-Sep-1999
C:Accession: A47556
R:Lustig, K.D.; Shiau, A.K.; Brake, A.J.; Julius, D.
Proc. Natl. Acad. Sci. U.S.A. 90, 5113-5117, 1993
A:Title: Expression cloning of an ATP receptor from mouse neuroblastoma cell: A:Reference number: A47556 MUID:93281707
A:Accession: A47556
A:Status: pre-filminary
A:Molecule type: mRNA
A:Residues: 1-373 <LUS>
A:COSS = references: GB:L14751; NID:9309457; PIDN:AAA39871.1; PID:9309458
C:Superfamily: ATP receptor P2u
C:Keywords: transmembrane protein
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Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-Sep-1999
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30.1%; Pred. No. 5.8e-22;
1ve 44; Mismatches 150;
   - human
intron 17 purinergic receptor P2Y5
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Best Local Similarity 30.8%
Matches 88; Conservative
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Best Local Similarity
Matches 98; Conserv
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A; Cross-references: GDB:134185; OMIM:182451
A; Map position: 14q13-14q13
A; Introns: #status absent
C; Superfamily: vertebrate rhodopsin
C; Keywords: G protein-coupled receptor; glycoprotein; hormone receptor; lipoprotein;
E; 58-44 Domain: transmembrane #status predicted <TM2>
E; 132-120/Domain: transmembrane #status predicted <TM3>
E; 132-155/Domain: transmembrane #status predicted <TM3>
E; 132-155/Domain: transmembrane #status predicted <TM5>
E; 202-250/Domain: transmembrane #status predicted <TM6>
E; 202-250/Domain: transmembrane #status predicted <TM6>
E; 202-250/Domain: transmembrane #status predicted <TM6>
E; 132-250/Domain: transmembrane #status predicted <TM6>
E; 133-250/Domain: transmembrane #status predicted <TM6
E; 133-25
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A;Title: Cloning and functional characterization of a family of human and mouse somat A;Reference number: A41795; MUID:92108031
A;Accession: A41795
       protein-coupled receptor; hormone receptor; transmembrane protein
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C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 24-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                   84 LRYAKMKTATNIYILNLAIADELLMLSVPFLVTSTL-LRHWPFGALLCRLVLSVDAVNMF 142
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                                                                                                                                                                                                                                                                                                24 GACSRGPGSGAADGMEEPGRNASQNGTLSEGQGSAILISFIYSVVCLVGLCGNSMVIYVI 83
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A; Residues: 1-391 <YAM>
A; Cross-references: GB: M81829; NID: 9307433; PIDN: AAA58247.1; PID: 9307434
A; Note: sequence extracted from NCBI backbone (NCBIN:74767, NCBIP:74768)
                                                                                                                                                                                                                                                                                                                                                                                 41 CFHMKTWKPSTVYLFNLAVADFLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRA
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                                                                            Query Match
16.6%; Score 307; DB 2; L
Best Local Similarity 25.7%; Pred. No. 9.9e-21;
Matches 85; Conservative 62; Mismatches 130;
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           C; Keywords: G
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R;O'Carroll, A.M.; Lolait, S.J.; Konig, M.; Mahan, L.C.
MOL. Pharmacol. 44, 1278, 1993
A;Title: Affile: Cloning and expression of a pituitary somatostatin receptor with pref A;Reference number: I57949; MuID:94088493
A;Accession: I57949
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Cispecias; Musculus (house mouse)
Cispecias; Musculus (house mouse)
Cispecias; Musculus (house mouse)
Riyamada, Y.; Post, S.R.; Wang, K.; Tager, H.S.; Bell, G.I.; Selno, S. Proc. Natl. Acad. Sci. U.S.A. 89, 251-255, 1992
Proc. Natl. Acad. Sci. U.S.A. 89, 251-255, 1992
A:Title: Cloning and functional characterization of a family of human and mo A:Title: Cloning and functional characterization of a family of human and mo A:Tacus: nucleic acid sequence not shown
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Molecule type: DNA
A:Cross-references: GB:MB1831; NID:g201058; PIDN:AAA58255.1; PID:g201059
C; Superfamily: vertebrate rhodopsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: mRNA
A;Residues: 309-363 <PEN>
A;Cross-references: EMBL:X74828; NID:g433911; PIDN:CAA52825.1; PID:g433912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              159 AAVWVFSLLMSLPLLV--FADVQEGWGTCNLSWPEPVGLWGAAFITYTSVLGFFGPLLVI 216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   217 CLCYLLIVVKVKAAGMRVGSSRRRSEPKVTRMVVVVLVFVGCWLPFFIVNIVNLAFTL 276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ::| | :: :| || : : | || 39 LVPVLYLLVCTVGLSGNTLVIYVVLRHAKMKTVTNVXILNLAVADVLFMLGLFFLATQNA 98
                                                                                                                                                                                                                                                                                                                                                                                                        A.Status: preliminary; translated from GB/EMBL/DDBJ
*Molecule type: mRNA
A;Residues: 341-363 < CCA2>
A;Cross-references: GB:S67370; NID:g455947; PIDN:AAB29371.1; PID:g455948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A:Experimental source: pituitary
R:Penetta, R: Greenwood, M: Patel, Y.C.
submitted to the EMBL Data Library, August 1993
A:Description: Correction of the nucleotide and amino acid sequence of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53; Mismatches 148;
                                                                         A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-363 <CCA1>
A; Reference number: 157940; MUID:93125499
A; Accession: 157940
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A; Accession: S39244
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angiotensin II receptor type 1 - bovine
C;Species: Bos primigenius indicus x Bos primigenius taurus (cattle)
C;Decies: Bos primigenius indicus x Bos primigenius taurus (cattle)
C;Decies: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Nov-1999
C;Accession: S15403
R;Saski, K.; Yamano, Y.; Bardhan, S.; Iwai, N.; Murray, J.J.; Hasegawa, M.; Matsuda, Mature 351, 230-233, 1991
A;Title: Cloning and expression of a complementary DNA encoding a bovine adrenal angla A;Reference number: S15403
A;Accession: S15403
A;Accession: S15403
A;Molecule type: mRNA
A;Rossion: S15403
A;Rossio
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90 MEYRWPFGNYLCKIASASVSFNLYASVFLLTCLSIDRYLAIVHPMKS-RLRRTMLVAKVT 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3LFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNTISTRVAAGIV 136
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LKKAYEIQKNKPRKDDIFKIILAIVLFFFFSWVPHQIFTFMDVLIQ 267
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16.4%; Score 304.5; DB 2;
Best Local Similarity 24.9%; Pred. No. 1.5e-20;
Matches 81; Conservative 68; Mismatches 143;
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A;Map position: 17924-18924
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279 VFVICWMPFYVVQLV
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209 -LIILTSYTLIWKT
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                                                                                                                                                                                                                   SFQRI-LC 339
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A; Ross references: GBrafoll4; GB:X61630; NID:956309; PIDN:CAA44193.1; PID:956310
A; Richard Source: brain
A; Note: it is uncertain whether Met-1 is the initiator or whether translation is initiat
B; Li, X.J.; Forte, M.; North, R. A.; Ross, C.A.; Snyder, S. H.
J. Biol. Chem. 267, 21307-21312, 1992
A; Title: Cloning and expression of a rat somatostatin receptor enriched in brain.
A; Reference number: A45102; MUID:93016064
A; Reference number: A45102; MUID:93016064
A; Reference number: A45102
A; Status: preliminary; not compared with conceptual translation
A; Wolecule type: nucleic acid
A; Residues: 1-391 <LII.>
A; Reperimental source: brain
A; Note: sequence extracted from NCBI backbone (NCBIP:116692)
C; Superfamily: vertebrate rhodopsin
C; Reywords: G protein-coupled receptor; glycoprotein; receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nalternate names: probable G-protein-coupled receptor; SRIF receptor
C;Species: Rattus norvegicus (Norway rat)
C;Date: (03-Aug-1992 #sequence_revision 03-Aug-1992 #text_change 24-Nov-1999
C;Accession: A39297; A45102; S20088
R;Meyerhof, W.; Paust, H.J.; Schoenrock, C.; Richter, D.
A)MA Cell Biol. 10, 689-694, 1991
A;Title: Cloning of a cDNA encoding a novel putative G-protein-coupled receptor expresse
A;Reference number: A39297; MUID:92096119
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                                                                                       VNTISTRVAAGIVCTLWALVILGTVYLLLENHLCV-QETAVSCESFIMESANGWHD---- 178
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; Pred. No. 1.4e-20;
62; Mismatches 128;
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C.Superfamily: vertebrate rhodopsin
C.Superfamily: vertebrate rhodopsin
C.Keywords: G protein-coupled receptor; glycoprotein; hormone receptor; lipoprotein; phc
F;44-69/Domain: transmembrane #status predicted <TM1>
F;80-105/Domain: transmembrane #status predicted <TM3>
F;117-138/Domain: transmembrane #status predicted <TM4>
F;128-130/Domain: transmembrane #status predicted <TM4>
F;25-235/Domain: transmembrane #status predicted <TM6>
F;28-115/Domain: transmembrane #status predicted <TM6>
F;28-115/Domain: transmembrane #status predicted <TM6>
F;28-115/Domain: transmembrane #status predicted <TM6>
F;32,23,331/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;15-193/Disulfide bonds: #status predicted
F;250/Binding site: phosphate (Ser) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                  16.3%; Score 302.5; DB 2; Length 369; 29.8%; Pred. No. 2.4e-20; Live 50; Mismatches 135; Indels 27
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Best Local Similarity 29.88
Matches 90; Conservative
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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd
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US-09-299-843A-44
US-09-099-843A-44
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A HUMAN 7-TRANS
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                                                                  Sequence 6, M
Sequence 6, M
Sequence 6, M
Sequence 6, M
Sequence 9, M
Sequence 2, M
Sequence 2, M
Sequence 2, M
Sequence 2, M
Sequence 3, M
Sequence 8, M
Sequence 8, M
                                                                                                                                                                                                                                                                                                                                             Sequence 6
Sequence 1
Sequence 2
                              Sequence
                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/08955713

Patent No. 595508

GENERAL INFORMATION:
APPLICANT: SATHE;
APPLICANT: BERGSMA, DERK
APPLICANT: HALSEY, WENY
TITLE OF INVENTION:
CORRESPONDENCES: 4

CORRESPONDENCE ADDRESS:
ADDRESSE: RAINER & PRESTIA
STREET: P.O. BOX 980
CITY: VALLEY FORGE
STATE: PA
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US-08-476-976-5
US-08-474-410-5
US-08-097-98-6
US-08-476-000-6
US-08-476-976-6
US-08-474-410-6
US-08-474-410-6
US-08-417-410-6
US-08-417-103-1
US-08-120-601B-9
US-08-121-103-14
US-08-120-601B-8
US-08-417-103-16
US-08-417-103-16
US-08-417-103-16
US-08-417-103-16
US-08-418-673-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELERAX: 610-407-0701
TELEX: 846169
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 423 amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 28.5%
Best Local Similarity 39.2%
Matches 115; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                single
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    STRANDEDNESS:
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US-08-955-713-2
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138 TEWALVILGTVYLLLENHLCVQETAVSCESFIM----ESANGWHDIMFQLEFFMPLGIIL 193
                                                                                                                                                                                                                                                                                                                                    FCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSV---SARLYFLWTVPSS 250
                                                                                                             78 RRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNTISTRVAAGIVC 137
18 MPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMICLPFRTDYYLR 77
                                  6 LAPILALEFYLGLVGNSLALFIFCIHTRPWTSNTVFLVSLVAADFLLISNLPLRVDYYLL 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT TIPE: LUSKELLE
COMBUTER: IBM COMPATIBLE
COPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/130,749
FILING DATE: US/09/130,749
FILING DATE: UNKNOWN
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
TILING DATE: CURROWN>
FILING DATE: CURROWN>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: SHABON, USMAN ELSHOURBAGY, NABIL TITLE OF INVENTION: MOLECULAR CLONING OF A 7TM RECEPTOR (GPR31A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 251 A---CDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSF 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEDICTQLFHG---SLAFTYLNSVLDPVLYCFSSPNF 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Score 451.5; DB
; Pred. No. 1.1e-31
61; Mismatches 12
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REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GP-70513
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-130-749-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS: ADDRESSEE: RATHER & PRESTIA
STREET: P.O. BOX 980
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TELEPHONE: 610-407-0700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/09130749 Patent No. 6031090 GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 610-407-0701
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Best Local Similarity 34.44
Matches 101; Conservative
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                                                      LMICLPFRIDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHA 123
                                                                                                                                                                                                                                              124 VNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQE-TAVSCESFIM----ESANGWHD 178
                                                                                                                                                                                                                                                                                   179 IMFQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSV- 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                         GSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --SARLYFLWTVPSSA---CDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSF 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 476;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GERERAL INFORMATION:
APPLICANT: SATHE, GANESH
APPLICANT: MOONEY, JEFFREY
APPLICANT: HALSEY, WENDY
ITILE OF INVENTION: CDNA CLONE HEOAD54 THAT ENCODES
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: RATHER & PRESTIA
STREET: PO. BOX 980
CITY: VALLEY FORGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FASTSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION WINBER: US/08/955,713
FILING DATE: 23-0CT-1997
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 60/050,124
FILING DATE: 18-JUN-1997
ATTORNEY/AGENT INFORMATION:
ANDER FORMER AND AND ADDRESS AND AND ADDRESS 
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REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GH-70087
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/08955713
Patent No. 5955308
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Simi
Matches 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 2
US-08-955-713-4
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126 LSPQAALGVSGLVWLLAVALTCPGLEISE--AAQNSTRCHSF-YSRADGSFSIIWQEALS 182
                   67 CLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNT 126
                                                                                                                                                                   127 ISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANG----WHDIMF
                                                                                                                                                                                                           183 CLQFVLPFGLIVFCNAGIIRALQKRLREPEKQPKLQRAQALVTLVVVLFALCFLPCFLAR
                                                                                                                                                                                                                                                                    243 VLMHIFQNLGSCRALCAVAHTSDVTGSLTYLHSVLNPVVYCFSSPTFRSSYRRV 296
                                                                                                                                                                                                                                                  241 --LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKL 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        G PROTEIN COUPLED RECEPTOR PROTEIN, PRODUCTION, AND USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/513,974B
FILING DATE: 14.5EP-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: PCT/JP95/01599
FILING DATE: 10-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-093889
FILING DATE: 19-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-09388
                                                                                                                                                                                                                                                                                                                                                                              Sequence 374, Application US/08513974B Patent No. 6114139 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 02-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NOTA:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236356
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: JP 7-057186 FILING DATE: 16-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-007177
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30-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JP 6-326611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 20-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tetsuya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Fukusumi, Shoji
APPLICANT: Ohgi, Kazuhiro
                                                                                                                                                                                                                                                                                                                                                                                                                                        Hinuma, Shuji
Hosoya, Masaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hosoya, Mass
Fujii, Ryo
Ohtaki, Tets
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: G
TITLE OF INVENTION: PR
NUMBER OF SEQUENCES: 3:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                               US-08-513-974B-374
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                                                                              182 QLEFFMPLGIILFCSFKIVWSLRRR-QQLARQARMKKAİRFIMVVAIVFITCYLPSVSAR 240
                                                                                                                                                                                                                              67 CLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNT 126
                                                                                                                                127 ISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANG-----WHDIMF 181
7 CRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMI 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     243 VLMHIFQNLGSCRALCAVAHTSDVTGSLTYLHSVLNPVVYCFSSPTFRSSYRRV 296
                                                                                                                                                                                                                                                                                  241 -- LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKL 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 319;
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                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/09130749
Fatent No. 6031344
GENERAL INFORMATION:
APPLICANT: SHABON, USMAN
TITLE OF INVENTION: MOLECULAR CLONING OF A 7TM
TITLE OF INVENTION: RECEPTOR (GPR31A)
WUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: RAINER & PRESTIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 451.5; DB 3; Pred. No. 1.1e-31; 61; Mismatches 121.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEC for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US/09/130,749
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GP-7
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0701
TELEFAX: 610-407-0701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: RATNER & PRESTIA
STREET: P.O. Box 980
CITY: Valley Forge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24.48;
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 319 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-130-749-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: P
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                US-09-130-749-2
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Best Local (
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PatentIn Release #1.0, Version #1.30
                                FILING DATE: 15-NOV-1995
CLASSIFICATION 10435
ATORNEX/AGENT INFORMATION:
NAME: Adler, Reld G
REGISTRATION NUMBER: 30,988
REPERENCE/DOCKET NUMBER: 0444!
TELECHONE: 202-467-7000
TELEFRAX: 202-467-700
                                                                                                                                                                                                                                                        LENGTH: 373 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                        CURRENT APPLICATION DATA
                                                                                                                                                                                                   TELEFAX: 202-467-7176
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Sim
Matches 92;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IMFQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLP--- 235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----SVSARLYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNK 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18 MPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMICLPFRTDYYLR 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              163 LVWALVVAVIAPILFYSGIGVRRNKTITCYDTTADEYLRSYFVYSMCTTVFM-----
                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 362;
                                                                                                                                                                                                                                                                                                                                                                                                                                        20.0%; Score 371; DB 3; Length 36
29.1%; Pred. No. 1.2e-24;
tive 60; Mismatches 128; Indels
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Patent No. 5871963
GENERAL INFORMATION:
GENERAL TOOLLEY, Pamela B.
APPLICANT: Jantzen, Hans-Michael
TITLE OF INVENTION: NOVEL PURINERGIC RECEPTOR NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: MORGAN, LEWIS & BOCKIUS LLP
1800 M Street, N.W.
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ZIP: 20036-5869
ZIP: 20036-5869
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                 APPLICATION NUMBER: JP 6-189273
FILING DATE: 11-AUG-1945
FRIGNR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189272
FILING DATE: 11-AUG-1994
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: JP 6-189274 FILING DATE: 11-AUG-1994 PRIOR APPLICATION DATA:
                                                                                                                                                               NAME: Resnick, David S.
REGISTRATION NUMBER: 34,235
REFRENCE/DOCKET NUMBER: 4575;
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
                                                                                                                                                                                                                                                      TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 374:
SEQUENCE CHARACTERISTICS:
LENGTH: 362 amino acids
TYPE: amino acids
STRANDEDNESS:
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Best Local Similarity 29.1.
Best Local Similarity 29.1.
Chest Local Similarity 29.1.
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MOLECULE TYPE: peptide
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STATE: D.C.
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241 LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK 300
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                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                  18 MPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMICLPFRTDYYLR 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLP----SVSAR
                                                                                                                                                                                                                                                                                                                             Length 373;
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Petent No. 6663582
CENERAL INFORMATION:
APPLICANT: Conley, Pamela B.
TILE OF INVENTION: NOVEL PURINERGIC RECEPTOR
INTER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
STREET: 1800 M Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/749,707
                                                                                                                                                                                                                                                                                                                                DB 2;
                                                                                                                                                                                                                                                                                                                             19.6%; Score 362.5; DB 2; 27.5%; Pred. No. 6.5e-24; Live 68; Mismatches 140;
044481-5010-00-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301 QPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSD 335
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48 VVFILGLITNSVSLEVECFRAKARSETAIFITNLAVSDLLFVCTLPFKI-FYNFNRHWPF 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84 GDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNTISTRVAAGIVCT-LWAL 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   195 CSFKIVWSLRRRQQLAR-QARMKKATRFIMVVAIVFITCYLPSVSARLYFLWTVPSSAC- 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           253 ----DPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPK-FYNKLKICSLKPKQPGHSK 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      143 VILGTVYLLLENHLCVQETAVSC-ESFIMESANGWHDIMFQLE-----FFMPLGIILF 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24 VAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMICLPFRTDYYLRRRHWAF 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 44, Application US/08153848
Patent No. 5759804
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: No. 5759804el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Marshall, O'Toole, Gerstein, Murray
                                                                                                                                                                                                                                                                                                                                                                                                                                                         18.7%; Score 346.5; DB 3; 31.2%; Pred. No. 1.5e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52; Mismatches 128;
                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: William T. Han,
REGISTRATION NUMBER: 34,344
REGISTRATION NUMBER: ATG50043
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 370 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95; Conservative
                                                                                                                                                                                                                     TELEFAX: 610-270-4060
                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
                            PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bicknell
                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  307 TQRP 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        336 TETP 339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-153-848-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-781-250-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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Patent No. 601087
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Sathe, Ganesh
APPLICANT: Van Horn, Stephanie
APPLICANT: Wac, Joyce Yue
TITLE OF INVENTION: CDNA CLONE HEBCS41 THAT ENCODES A NOVEL 7-TRANSMEMBRAN
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham
STREET: 709 Swedeland Road
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                       7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          138 TLWALVILGTVYLLLENHLCVQET-AVSC-----ESFIMESANGWHDIMFQLEFFM 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            174 LVWLIVVVGISPILFYSGTGIRKNKTITCYDTTSDEYLRSYFIYSM-----CTTVAMFCV 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   229 PLVLILGCYGLIVRALIYK-DLDNSPLRRKSIYLVIIVLTVFAVSYIPFHVMKTMNLRAR 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78 RRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNTISTRVAAGIVC 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18 MPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMICLPFRTDYYLR 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        188 PLGIILFCSFKIVWSLRRRQQLARQARWKKATRFIMVVAIVFITCYLP----SVSAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     288 LDF-QTPEMCAFNDRVYATYQVTRGLASLNSCVDPILYFLAGDTFRRLSR------
                                                                                                                                                                                                                                                                                                                                                                                               DB 3; Length 373;
                                                                                                                                                                                                                                                                                                                                                                                          Query Match
19.6%; Score 362.5; DB 3; Length 3
Best Local Similarity 27.5%; Pred. No. 6.5e-24;
Matches 92; Conservative 68; Mismatches 140; Indels
FILING DATE: 15-NOV-1996
CLASSIFICATION: 536
TTORNEY/AGENT INFORMATION:
NAME: AAGENT REIGHT 810
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 044481-5010-01-US
TELECOMMUNICATION INFORMATION:
TELECHONE: 202-467-7000
TELEFAX: 202-467-7000
TELEFAX: 202-467-7000
TELEFAX: 203-467-7156
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 373 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: DOS
SOFTWARE: FastSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,250
FILING DATE: 10-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301 QPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSD 335
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MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-749-707-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM:
                                                                                                                                                                                                                                                             TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
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258 YVLHYRSHGASCATQRILALANRITSCLTSLNGALDPIMYFFVAEKFRHALCNL-LCGKR 316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         127 ISTR--VAAGIVCT-LWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIMFQL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      200 AFTFPFITTVTCYLLIIRSL--RQGLRVEKRLKTKAVRMIAIVLAIFLVCFVPYHVNRSV 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YFL-WTVPSSACDPSVHGAL--HITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLK 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 CRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMI 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      184 EFFMPLGIILFCSFKIVWSLRRRQQLARQARMK-KATRFIMVVAIVFITCYLP-SVSARL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 44, Application US/09299843A
Patent No. 6107475
GENERAL INFORMATION
APPLICANT: Godiska, Ronald
APPLICANT: Godiska, Ronald
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 30.5%; Pred. No. 1.1e-21;
Matches 97; Conservative 54; Mismatches 153; Indels
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OPERATING SYSTEM: DOS
SOFTWARE: FastESD for Windows Version 2.0
CURRET APPLICATION DATA:
APPLICATION NUMBER: US/08/812,871
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/812,871
FILING DATE:
ATTORNEY-AGENT INFORMATION:
NAME: B1111ngs, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0237 US
TELEPHONE: 415-85-0555
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 anino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  299 PKQPGHSKTQRPEEMPIS 316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
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LIBRARY: General 992700
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67 CLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNT 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23 CGQETPLENMLFASFYLLDFILALVGNTLALMLFIRDHKSGTPANVFLMHLAVADLSCVL 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 CRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMI 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: ANOTOMICAL INCOMES, Janice
APPLICANT: Guegler, Karl
APPLICANT: Guegler, Karl
APPLICANT: Muzong Cheng
TITLE OF INVENTION: NOVEL HUMAN CHEMOKINE RECEPTOR-LIKE
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSE: Incyte Pharmaceuticals, Inc.
STREET: Palo Alto
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 18.1%; Score 336; DB 1; Length 33 Best Local Similarity 30.5%; Pred. No. 1.1e-21; Matches 97; Conservative 54; Mismatches 153; Indels
                                          FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5759604and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/COCKET NUMBER: 31794
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (312) 474-6300
TELEFAX: 25-3856
INFORMATION FOR SEQ ID NO: 444:
SEQUENCE CHARACTERISTICS:
     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/153,848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/08812871 Patent No. 5955303 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   299 PKOPGHSKTORPEEMPIS 316
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COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                317 LKGPPPSFEGKTNESSLS 334
                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 339 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: protein US-08-153-848-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-812-871-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      242
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184 EFFMPLGIILFCSFKIVWSLRRRQQLARQARMK-KATRFIMVVAIVFITCYLP-SVSARL 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                127 ISTR--VAAGIVCT-LWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIMFQL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 CRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMI 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23 CGQETPLENMLFASFYLLDFILALVGNTLALWLFIRDHKSGTPANVFLMHLAVADLSCVL 82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 339;
                                                                                    STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                            COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
18.1%; Score 336; DB 4; L
Best Local Similarity 30.5%; Pred. No. 1.1e-21;
Matches 97; Conservative 54; Mismatches 153;
                                            ADDRESSEE: Marshall, O'Toole, Gerstein,
                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 08/153,848
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: NO. 6348574and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/088,337B
FILING DATE: 01-Jun-1998
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 44:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
PCT-US93-11153-44
Sequence 44, Application PC/TUS9311153
, GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
                                                                                                                                                 COUNTRY: USA ZIP: 60606 COMPUTER READABLE FORM: MEDIUM TYPE: FLOPPY disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (312) 474-0448
TELEX: 25-386
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 339 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
NUMBER OF SEQUENCES: 66
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                     CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
                                                                                                           CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-088-337B-44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          140 LKLRRPLYAHLACAFLWVVAVAMAPLLVSPQTVQTNHTVVCLQLYREKASHHALVSLAV 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 CRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMI 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23 CGOETPLENMLEASFYLLDFILALVGNTLALMLEIRDHKSGTPANVFLMHLAVADLSCVL 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 44, Application US/09088337B
Patent No. 6348574
GENERAL INFORMATION:
APPLICANT: Godska, Ronald
Gray, Patrick W.
Schweikart, Vicki L.
TITLE OF INVENTION: No. 6348574el Seven Transmembrane Receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EFFMPLGIILFCSFKIVWSLRRRQQLARQARMK-KATRFIMVVAIVFITCYLP-SVSARL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54; Mismatches 153; Indels
                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: J111 E. Uhl
REGISTRATION NUMBER: 43,213
REFERENCE/DOCKET NUMBER: 27866/32059B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-6300
                                                                                                                                                      APPLICATION NUMBER: US/09/299,843A
                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 08/153,848
FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/088,337
FILING DATE: 01-JUN-1998
PRIOR APPLICATION DATA:
                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 339 amino acids
TYPE: amino acid
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-088-337B-44
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GENERAL INFORMATION:
APPLICANT: LI, YI
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ZIP: 07068
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      184 EFFMPLGIILFCSFKIVWSLRRRQQLARQARMK-KATRFIMVVAIVFITCYLP-SVSARL 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YFL-WTVPSSACDPSVHGAL--HITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLK 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 CRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMI 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23 CGQETPLENMLFASFYLLDFILALVGNTLALMLFIRDHKSGTPANVFLMHLAVADLSCVL 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18.1%; Score 336; DB 5; Length 339; 30.5%; Pred. No. 1.1e-21; tive 54; Mismatches 153; Indels
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OT INVENTION: Novel Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
                                                                                                                                                6300 Sears Tower, 233 South Wacker Drive
                                                                                                           ADDRESSEE: Marshall, O'Toole, Gerstein, Murray ADDRESSEE: Bicknell
                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/11153
                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (312) 474-6300
TELERX: (312) 474-6448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Noland, Greta E. REGISTRATION NUMBER: 35,302 REFERENCE/DOCKET NUMBER: 31.
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     299 PKQPGHSKTQRPEEMPIS 316
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Matches 97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US93-11153-44
                                                                                                                                                  STREET: 6300 See CITY: Chicago STATE: Illinois
                                                                                                                                                                                                            USA
                                                                                                                                                                                                      COUNTRY: US
ZIP: 60606
                                                                                                                                                                                                                                                                                                                                                                              FILING DATE
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PCT-US95-07180-2
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Sequence 2, Application PC/TUS9507180

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127 ISTR--VAAGIVCT-LWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIMFQL 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    200 AFTFPRITTVTCYLLIIRSL--RQGLRVEKRLKTKAVRMIAIVLAIFLVCFVPYHVNRSV 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         242 YFL-WTVPSSACDPSVHGAL--HITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLK 298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 CRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMI 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18.1%; Score 336; DB 5; Length 339
30.5%; Pred. No. 1.1e-21;
.ive 54; Mismatches 153; Indels
                                                                                                                                                             ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI, ADDRESSEE: STEWART & OLSTEIN STREET: 6 BECKER FARM ROAD STREET: 6 BECKER FARM ROAD STATE: NJ
                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
APPLICANT: LI, YI
APPLICANT: GOCAYNE, JEANINE D
APPLICANT: RUBEN, STEVEN M
TITLE OF INVENTION: G-PROTEIN RECEPTOR HIBEB69
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 06-JUNE-1995
CLASSIFICATION:
ATTONNEY, FAGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 30,073
REFERENCE/DOCKET NUMBER: 325800-366
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEPHONE: 201-994-1744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SULTWARE.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07180
FILING DATE: 06-JUNE-1995
                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 15
US-08-467-948A-30
; Sequence 30, Application US/08467948A
; Patent No. 5998164
; GENERAL INFORMATION:
APPLICANT: LI, YI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     299 PKQPGHSKTQRPEEMPIS 316
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amino acid
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Best Local Similarity 30.55
Matches 97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear

MOLECULE TYPE: protein

PCT-US95-07180-2
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                APPLICANT: NI, JIAN
APPLICANT: GENTZ, REINER
APPLICANT: BULJ, CAROL J.
APPLICANT: SUTTON III, GRANGER G.
APPLICANT: ROSEN, CRAIG A.
TITLE OF INVENTION: POLYNUCleotides Encoding Human G-Protein
TITLE OF INVENTION: Coupled Receptor GRR2
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: STENE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2; Length 302;
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CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30
SOFTWARE: PAPLICATION DATA:
APPLICATION NUMBER: US/08/467,948A
FILING DATE: 06-010-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: PCT/US95/04079
FILING DATE: 30-MAR-1995
ATTORNEY/AGENT INFORMATION:
REFERENCE/OOCKET NUMBER: 1488.1140003/EKS/KLM
TELECPHONE: 202-371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 202-371-2600
TELEPKX: 202-371-2540
INFORMATION FOR SEQ ID NO: 30: SEQUENCE CHARACTERISTICS:
LENGTH: 302 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
CAO, LIANG
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Search completed: October 29, 2002, 04:55:15 Job time : 28 secs

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Perfect score:

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AJ300198 Mus muscu
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AR098624 Sequence
165543 Sequence
AX148166 Sequence
AX338078 Sequence
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AR107258 Sequence
Y12366 H.sapiens m
AC010976 Homo sapi
294155 H.sapiens m
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AL121935 Human DNA
AL353591 Homo sapi
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U65402 Human seven
                AX148182 Sequence
AX299705 Sequence
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E31721 CDNA clone
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (Jasse 1 to 1041)

Vogeli,G., Wood,L.S., Parodi,L.A., Hiebsch,R.R., Lind,P.,

Slightom,J., Schellin,K.A., Kaytes,P.S., Bannigan,C.M., Ruff,V.,

Sejlitz,T. and Huff,R.M.

Novel g protein-coupled receptors

Patent: WO 0136473-A 79 25-MAY-2001;

PHARMACIA & UPJOHN COMPANY (US)
    Sequence
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JOURNAL
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AUTHORS
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                  GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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Chen,R., Dang,H.T. and Lowitz,K.P. Endogenous and non-endogenous versions of human g protein-receptors
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Homo sapiens G protein-coupled receptor (GPR81) gene, complete cds. AF411110. BE411110.1 GI:16566325
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 TGGAGCCTGAGGCGGAGCAGCAGCTGGCCAGGCTCGGATGAAGAAGGCGACCCGG
                721 CTCTATTTCCTCTGGACGGTGCCCTCGAGTGCCTGCGATCCCTCTGTCCATGGGGCCCTG
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tive 0; Mismatches 0;
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/db_xref="taxon:9606"
294 c 278 g 26
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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adjunder, V. Vernet, C.A., Casman, S.J., Wolenc, A.R., Spadern
Padjuaru, M., Mishnu, V.S., Tchernev, V.T., Spytek, K.A., Li, L.
Baumgartner, J.C. and Gusev, V.Y.
Novel proteins and nucleic acids encoding same
Patent: WO 01/14904-A 1 11-OCT-2001;
Curagen Corporation (US)
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                                                                                                   TTCCAGCTGGAGTTCTTTATGCCCCTCGGCATCATCTTATTTTGCTCCTTCAAGATTGTT
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tive 0; Mismatches 0;
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299 c 279 g 261
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Lee, D.K., Nguyen, T., Lynch, K.R., Cheng, R., Vanti, W.B., Arkhitko, O., Lewis, T., Evans, J.F., George, S.R. and O'Dowd, B.F. Discovery and mapping of ten novel G protein-coupled receptor genes (2n4 58557) 11574155
                                                                                                                                                                                                                                                                                                                                                                               /product="G protein-coupled receptor"
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TRFINVVAIVFITCYLDSVSARLYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPL
                                                                                               Theses 1 to 1041)
Lee.D.K., Nguyen,T., Lynch,K.R., Cheng,R., Vanti,W.B., Arkhitko,O., Lewis,T., Evans,J.F., George,S.R. and O'Dowd,B.F.

Direct Submission.
Submitted (17-AUG-2001) Department of Pharmacology, University of Toronto, 8 Taddle Creek Rd. Rm. 4353, Toronto, Ont M5S 1A8, Canada Location/Qualifiers
1. 1041
//Organism="Homo: saplens"
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//chromosome="12"
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/product="G protein-coupled receptor"
<1. .>1041
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09-JAN-2002 ö Spaderna, S.K., Li, Li, L., Euteleostomi; 125 180 185 245 360 365 420 425 480 485 540 545 900 120 665 Gaps 65 9 GATTTCCTCCTTATGATCTGCCTGCCTTTTCGGACAGACTATTACCTCAGACGTAGACAC CTGCTCATTGTGGCCTTTGTGCTGGGCGCACTAGGCAATGGGGTCGCCCTGTGTGGTTTC 1 ATGTACAACGGGTCGTGCTGCCGCATCGAGGGGGACACCATCTCCCAGGTGATGCCGCCG GGGAGCATCGTGTTCCTTACGGTGGTGCTGCGGACAGGTATTTCAAAGTGGTCCACCCC CACCACGCGGTGAACACTATCTCCACCCGGGTGGCGGCTGGCATCGTCTGCACCCTGTGG GCCCTGGTCATCCTGGGAACAGTGTATCTTTTGCTGGAGAACCATCTCTGCGTGCAAGAG TTCCAGCTGGAGTTCTTTATGCCCCTCGGCATCATCTTATTTTGCTCCTTCAAGATTGTT TGGAGCCTGAGGCGGAGGCAGCTGGCCAGACAGGCTCGGATGAAGAAGGCCGACCCGG GATITICCTCCTTATGATCTGCCTGCCTTTTCGGACAGACTATTACCTCAGACGTAGACAC TGGGCTTTTTGGGGACATTCCCTGCCGAGTGGGGCTCTTCACGTTGGCCATGAACAGGGCC PAT ö Length 1050 1 (sites)
Majunder,K., Vernet,C.A., Casman,S.J., Wolenc,A.R., Sp
Padigaru,M., Mishnu,V.S., Tchernev,V.T., Spytek,K.A.,
Baumgartner,J.C. and Gusev,V.Y.
Novel proteins and nucleic acids encoding same
Patent: WO 0174904-A 3 11-OCT-2001;
Curagen Corporation (US) Craniata; Vertebrata; I Catarrhini; Hominidae; Indels linear Ouery Match 100.0%; Score 1041; DB 6; Best Local Similarity 100.0%; Pred. No. 3.5e-249; Matches 1041; Conservative 0; Mismatches 0; DNA ų 262 /organism="Homo sapiens" /db\_xref="taxon:9606" 298 c 279 g 265 AX338373 1050 bp Sequence 3 from Patent WO0174904 AX338373 Chordata; Primates; Location/Qualifiers GI:18128870 Homo sapiens Eukaryota; Metazoa; Mammalia; Eutheria; AX338373.1 ø human 셤

	421 GCCCTGGTCATCCTGGGAACAGTGTATCTTTCCTGGAGAACCATCTCTGCAAGAG 480	Db 643 TGGAGCCTGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	SULT 8 27635 CACATTGTTGAGTGGCACTGA 27635 AX277635 EINITION Sequence 1 from Pate CESSION AX277635 RSION AX277635 RSION AX277635.1 GI:16604 WORDS human. ORGANISM Homo sapiens Eukaryota; Metazoa; Mammalia; Eutheria; FERENCE 1 (sites)
Qy         661 TTCATCATGGTGGCAATTGTTCATCACATGCTACCTGCCCAGCGTGTCTGCTAGA         720           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	901 CAGCCAGGACACTCAAAAACCAAAGGCCGAAAGACAATTCGAACCTCGGTCGCCTCGCTCG	RESULT 7 AX305131 LOCUST LOCUST Sequence 11 from Patent W00187937. ACCESSION AX305131 G:17644766 ACCESSION AX305131. G:17644766 NUMBON AX305131. G:17644766 NERNON AX305131. G:1764766 NERNON AX305131. G:1764776 NERNON AX305131. G:176	Query Match         100.0%;         Score 1041;         DB 6;         Length 1083;           Best Local Similarity 100.0%;         Pred. No. 3.5e-249;         Matches 1041;         Op. 3.5e-249;           Matches 1041;         Conservative 0;         Mismatches 0;         Indels 0;         Gaps 0;           Qy         1 ATGTACAACGGTCGTGCGCGATCGAGGGGACACCATCTCCCAGGTGATGCCGCC         60           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII

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              CAGCCAGGACACTCAAAAACACAAAAGGCCGGAAGAGAGATGCCAATTTCGAACCTCGGTCGC
                                                   AGGAGTTGCATCAGTGTGGCAAATAGTTTCCAAAAGCCAGTCTGATGGGCAATGGGATCCC
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                                                                                                                                                                                                                                                        Ye,J.C., Cravchik,A.C., di Francesco,V.C. and Beasley,E.M Isolated human g-protein coupled receptors, nucleic acid nencoding human gport proteins, and uses thereof Patent: WO 0173029-A 3 04-0CT-2001;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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/db_xref="taxon:9606"
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Sequence 3 from Patent WO0173029,
AX299707 GI:17129251
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 Regulation of human hm74-like g prol
Patent: WO 0177320-A 1 18-OCT-2001;
Bayer Aktlengesellschaft (DE)
Location/Qualifiers
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481 ACGGCCGTTCCTGTGAGGCTTCATCATGGAGTCGCCAATGGCTGGATGACATCATG 510			<del></del>	· • • • • • • • • • • • • • • • • • • •		TITLE JOURNAL REFERENCE	TITLE	COMMENT													
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arlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., atovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Liu, J., Lichterge, O., Lieu, C., Liu, J., Liun, W., Lozado, R.J., Ludier, A., Lucier, R., Lunder, R., hwari, M., Mapua, P., Martin, R., Martindale, A., hwari, M., Mapua, P., Martin, R., Martindale, A., kassey, E., Mawhiney, E., McGod, M.P., Meador, M., Ker, M., Miner, G., Miner, Z., Mitchell, T., Mohabbt, K., Orris, S., Moser, M., Neal, D., Newtson, J., Newtson, N., Outedo, R., Pace, A., Payton, B., rez, L., Peters, L., Pickens, R., Primus, E., Payton, B., rez, L., Peters, L., Pickens, R., Primus, E., Payton, B., rez, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N., odergren, E., Sonaike, T., Sparks, A., Stanley, H., Stoaike, T., Sparks, A., Stanley, H., Stoaike, T., Sparks, A., Tamerisa, R., Sey, J., Taylor, P., Tamerisa, A., Tamerisa, R., Sey, J., Taylor, C., Taylor, P., Tamerisa, A., Thomas, N., Sward-Moore, S., Warren, R., Washington, C., Williamson, A., Wilson, D., and Gibbs, R., Wu, Y., Wu
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Lone name: R11-507N20
-- Summary Statistics
ng vector: Pisanid: M77789
ng vector: M3: L08821
ng vector: M3: L08821
y: Dye-primer Bodlpy: 31% of reads
y: Dye-terminator Big Dye: 69% of reads
y: Dye-terminator Big Dye: 69% of reads
y: Dye-terminator Big Dye: 69% of reads
program: Phrap; version 0.990329
s quality: 175811 bases at least Q40
s quality: 179678 bases at least Q20
d insert size: 176741; sum-of-contigs estimation
coverage: 0x in Q20 bases; agarose-fp estimation
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a working draft's sequence. It currently
c contigs. The true order of the pieces
and their order in this sequence record is
so between the contigs are represented as
t the exact sizes of the gaps are unknown.
ill be uddated with the finished sequence
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IAR-2000) Human Genome Sequencing Center, Department
id Human Genetics, Baylor College of Medicine, One
louston, TX 77030, USA
this sequence version replaced g1:13877178.
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sc-help@bcm.tmc.edu
Project Information
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ive 0; Mismatches 0;
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                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
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Center clone name: R11-334E6
Center clone name: R11-334E6
Sequencing vector: M13: L08821
Sequencing vector: M13: L08821
Chemistry: Dye-primer Bodipy: 8% of reads
Chemistry: Dye-terminator Big Dye: 92% of reads
Chemistry: Dye-terminator Dye-terminator
Consensus quality: 200352 bases at least Q30
Consensus quality: 200352 bases at least Q30
Estimated insert size: 205209; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                              NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a "working draft" sequence. It currently consists of 13 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                           Submitted (22-MAR-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Sep 30, 2001 this sequence version replaced g1:14861654.
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contig of 43017 bp in length
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                                                                                                                                                                       Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
------ Project Information
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 Unpublished
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Worley, K.C.
Direct Submission
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93563: 0
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Length 204062;
100.0%; Score 1041; DB 2; 100.0%; Pred. No. 5.1e-249;
                                       Mismatches
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0
                                         Conservative
                    Similarity
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1021 CACATTGTTGAGTGGCACTGA 1041

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PAT 08-JUN-2001
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 888)
Vogeli,G., Wood,L.S., Parodi,L.A., Hiebsch,R.R., Lind,P.,
Slightom,J., Schellin,K.A., Kaytes,P.S., Bannigan,C.M., Ruff,V.,
Sejlitz,T. and Huff,R.M.
Novel g protein-coupled receptors
Patent: WO 0136473-A 11 25-MAY-2001;
PHARMACIA & UPJOHN COMPANY (US)
                                                                                                                                                                                                                                                                                                                                                            780
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                                                                                                                                       841 TCAAGCCCCTCCTTTCCCAAATTCTACAAGCTCAAAATCTGCAGTCTGAAAACCCAAG
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                                                                                                                                                                                               GATTTCCTCCTTATGATCTGCCTGCCTTTTCGGACAGACTATTACCTCAGACGTAGACAC
   TGGAGCCTGAGGCGGAGCAGCAGCTGGCCAGGCTCGGATGAAGAAGGCGACCCGG
                                                            661 TTCATCATGGTGGTGGCAATTGTGTTCATCACATGCTACCTGCCCAGCGTGTCTGCTAGA
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Best Local Similarity 100.0%; Pred. No. 5.3e-211;
Matches 888; Conservative 0; Mismatches 0;
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Sequence 11 from Patent WO0136473.
AX147766
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/db_xref="taxon:9606"
254 c 231 g 229
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1. .888
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AX147766
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Majumder,K., Vernet,C.A., Casman,S.J., Wolenc,A.R., Spaderna,S.K., Padigaru,M., Mishnu,V.S., Treernev,V.T., Spytek,K.A., Li,L., Baumgartner,J.C. and Gusev,V.Y.
Novel proteins and nucleic acids encoding same
Patent: WO 0174904-A 4 11-OCT-2001;
Curagen Corporation (US)
Location(Qualifiers
                                                                                                                                                                            Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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.2e-248;
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Pred. No. 2.2e-
0; Mismatches
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/organism="Homo saplens"
/db_xref="taxon:9606"
318 c 295 g 275
                                                                                  Sequence 4 from Patent WO0174904.
AX338374
Db 16591 CACATTGTTGAGTGGCACTGA 16611
                                                                                                                                  AX338374.1 GI:18128871
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99.88;
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Best Local Similarity 99.8
Matches 1039; Conservative
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00   000	Match 35.5%; Score 369.2; DB 6; Length 1092; coal Similarity 64.0%; Pred. No. 1.7e-81; s 598; Conservative 0; Mismatches 318; Indels 18; Ga 1 ATCTACACGGTCGTCTCCGCATCGGGGGACACCATCTCCCAGGTGATCCCGCC 1 ATCACACAAGGACTCTTCTCTGTTCTCCAGGTATCTCCAGGTGATCCCGCC 1. THE HILL HILL HILL HILL HILL HILL HILL HI	157 TGTTTCCACCTCAAGTCCTGGAAATCCAGCCGGATTTCCTGTTCAACCTGGCATGGCT 216  181 GATTTCCTCTTATGATCTGCTGCTGCTTTTCGGACAGATTTACCTCAACGAGCATGGCT 240  217 GACTTTCTACTGATCATCTGCCTGCCTTCTGATGGACAAATGTGAGGCTTGGAC 276  241 TGGGCTTTTGGGACATTCCTGCCGAGGGGCTCTTCACGTTGGCCATGGAC 276  241 TGGGCTTTTGGGACATTCCTGCCGAGGGGCTCTTCACGTTGGCCATGAACAGGGCC 300  277 TGGAAGTTTGGGAACATCCTTACGGGTGTGGTGTTTATTTGGCAACCCCAG 336  311 GGGAGCATCGTTCCTTACGGGTGTGGTGGTGTATTAAAGTGGTCCACCC 360  11 111111111111111111111111111111111	337 GGCAGCATCATCTTCCTCACGGTGGCGGTAGACAGGTATTTCCGGGTGGTCCATCCC 396  361 CACCACGCGGTGAACATATCTCCACCGGGTGGCTGGCTGG	TTCCAGCTGGAGTTCTTTATGCCCCTGGCATCATTATTTTGCTCCTTCAGATTGTT TTCCTCCTGGAGTTCTTTATGCCCCTGGCCATCATCTTATTTTGCTCCTTCAGATTGTT TTCCTCCTGGAGTTCTTTCTGGCCCTGGGCATCATCTTTTTGCTCCTCAGATTATC TGGAGCCTGGAGGCGAGCAGCTGGCCAGCAGCTGGAGAAGAGGCGACCGG TGGAGCCTGCGGCAGCAGCAGCCAGCCGGCTGAGAGAGGCCACCGG TTCATCATGGTGGCAGAGCAATGGTTCATCATCATGCTACCTGCCTAGCTCTGCTAGAGAGCCATCACCGCCTAGAGAGCCATCATGTTCATCATGCTACTTCCTCCCAGCGTGCTCTGCTAGAGAGCCATCGCTAGTTTTCATCATGGTGGTGGCCATCGTCTTTGTCATTGCTTCTTTGTCATTGCTTCTTTGTCATTGCTTCTTTGTCATTGCTTCTTTGTCATTGCTTCTTTGTCATTGCTTCTTTGTCATTGCTTCTTTGTCATTGCTTCTTTGTCATTGCTTCTTTGTCATTGCTTCTTTGTCATTGTTTTCTTTGTTCTTTTTTCTTTTTTTT	754 ATCGCATCTTCTGGCTCCTGCACATCGGCACAGATTGTGAAGTGTACCGCTCG 813 766 GTCCATGGGCCCTGCACATAACCTTCACCTACATGAACAGCATGCTGGATCC 813 814 GTGGACTGGCCTTGACTCTCAGCTTCACCTACATGAACAGCATGCTGGACCC 873 826 CTGGTGTATTATTTTCAGCCCTCTTTCCCAAATTCTACAACAGCATCCTGGACCC 885 811   1   1   1   1   1   1   1   1   1
TGGGCTTTTGGGGACATTCCCTGCCGAGTGGGGCTCTTCACGTTGGCCATGAACAGGGCGCGGGGCGGGGGGGG	Ouer Best Matc		qa		Db Qy Db Qy Db Db Db AX3355 LOCUS
	TGGGCTTTTGGGGACATTCCCTGCCGAGTGGGGCTCTTCACGTTGGCCATGAACAGGGCC	GCCCTGGTCATCCTGGGAACAGTGTATCTTTTGCTGGAGAACCATCTCTGCGTGCAAGAG ACGGCCGTCCTCGTGAGAGCTTCATCATGAGGTCGGCCAATGGCTGGC	TGGAGCCTGAGGCGGAGGCAGCAGCCAGACAGGCTCGGATGAAGAAGGGGACCGG TTCATCATCATGATGGTGGCAATTGTTCATCACATGCTACCTGCCCAGCGTGTTGTTGTTCATCATGATGCTACCTGCCCAGCGTGTTGTTGTTGTTCATCATGATGCTACCTGCCCAGCGTGTTGTTGTTCATCATGATGCTACTTGCCCAGCGTGTTGTTGTTCATCATGATGCTGCCCAGCGTGTTGTTGTTGTTCATCATGATGCTGCCTGC	TCAAGCCCTCCTTCCCAAATTCTACAACAGCTCCAAATCTGCAGTCTGAAACCCAA IIIIIIIIIIIIIIIIIIIIIIIIIIIIII	AXI48194.1 GI:14347090 human. Homo sapiens ENKaryord; Metazoa; Chordata; Craniata; Vertebrata; Euteli ENKaryord; Metazoa; Chordata; Catarrhini; Hominidae; Homo 1 (bases 1 to 1092) Chen, R., Dang, H.T. and Lowitz, K.P. Endogenous and non-endogenous versions of human g protein receptors Patent: WO 0136471-A 35 25-MAY-2001; Arena Pharmaceuticals, Inc. (US) Location/Qualifiers 1 . 1092 /organism="Homo sapiens" /db_xref="taxon:9606" 223 a 320 c 273 g 276 t

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994 TGCCTCCAGAGGAAGATGACAGGTGAGCCAGATA 1027
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Cancer gene determination and therapeutic screening using signature
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                                                      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                   1 (sites)
Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,
Horrigan, S., Soppet, D.R. and Weaver, Z.
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                                                                                                                                         Patent: WO 0194629-A 6104 13-DEC-2001
Avalon Pharmaceuticals (US)
Location/Qualifiers
1..2051
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Pred. No. 4.5e
0; Mismatches
 Sequence 6104 from Patent WO0194629
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/db_xref="taxon:9606"
530 c 525 g 520
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721 CTCTATITCCTCTGGACGGIGCCCTC
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Search completed: October 29, 2002, 03:17:28 Job time : 2068 secs

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES			ΙD	AAS12581	AAS07946	AAH51008	ABA81529	ABA81530	AAD26371	AAS18501	AAS12582	ABA81531
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The present invention relates to the isolation of a novel human G-protein coupled receptor (GPCR) which is related to the chemokine receptor subfamily. The CDNA and gene sequences encoding for GPCR are also given in the invention. The sequences of the invention are useful to diagnosing and treating diseases or conditions mediated by human proteinses. Such diseases include hyperpoliferative disorders.

(e.g. hyperplasia), neurological disorders (e.g. Parkinson's disease), psychiatric diseases (e.g. schizophrenia), inflammatory disorders (e.g. adult respiratory distress syndrome, ARDS). The GPCR protein is also useful for identifying a modulator of the expression of the protein. It also serves as a target for identifying agents for use in mammallan therapeutic applications, e.g. a human drug, particularly modulating a biological or pathological assays. GPCR is also useful in diagnosing a disease or predisposition to a disease mediated by the peptide, in pharmacogenomic nallysis. The sequence encodes for the novel human GPCR the invention.
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                                                                                             Novel human G-protein coupled receptor proteins and nucleic acid molecules encoding the protein for use in developing human therapeutics and diagnostic compositions and for identifying modulators of the
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                                                                                                                                                                                                                                                                                                                                                                                                             Human cDNA encoding G-protein coupled receptor, hRUP19.
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G protein-coupled receptor; nGPCR; seven transmembrane receptor; signal transduction; schizophrenia; thyroid disorder; renal failure; rheumatoid arthritis; CNS disorder; infection; metabolic disease; cardiovascular disease; proliferative disorder; hormonal disorder; heurological disorder; neuronal disorder; Alzhelmer's disease; cancer; attention deficit hyperactivity disorder/attention deficit disorder; Parkinson's disease; migraine; senile dementia; inflammatory disease; rheumatoid arthritis; autolmmune disorder; respiratory allment;
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                                                                                                                                                                                                                                                                                                                                                          Endogenous and non-endogenous versions of human G-protein coupled receptors for direct identification of candidate compounds as agonists, inverse agonists or partial agonists for use as therapeutic agents -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence encodes a human G-protein coupled receptor (GPCR)
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100.0%; Pred. No. 0;
:ive 0; Mismatches
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                                          10 APR-2000; 20000S-0195091

10 APR-2000; 20000S-0196078

28 APR-2000; 20000S-0200419.

12-JUN-2000; 2000US-0203630.

12-JUN-2000; 2000US-0210741.

12-JUN-2000; 2000US-0210982.

21-AUG-2000; 2000US-0210982.

26-SEP-2000; 2000US-0235418.

26-SEP-2000; 2000US-0235779.

20-OCT-2000; 2000US-023372.
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                 2000US-0189259
2000US-0195898
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Best Local Similarity 100.
Matches 1041; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to novel G protein-coupled receptors (nGPCRx; where x is 1, 3, 4, 5, 9, 11, 12, 14-18, 20, 21, 22, 24, 27, 28, 31-38, 40, 41, 55-60) and their coding sequences in the present c sequence is the coding sequence sort of protein-coupled receptor. G sequence is the coding sequences are useful for c signal transduction. The nGPCRx coding sequences are useful for signal transduction. The nGPCRx coding sequences are useful for c screening a human to diagnose a disorder affecting the brain or a genetic predisposition, specifically schizophrenia. nGPCRx are useful for identifying compounds useful for treating schizophrenia. Detection of nGPCRx in a sample is useful as diagnostic tool for diseases or identified is useful as a diagnostic tool for diseases or disorders e.g. thyroid disorders, renal failure, rheumatoid arthritis, CNS disorders, infections such as HIV-1, metabolic and cardiovascular disorders, infections deficit disorders, moditators of nGPCRx activity have the utility for treating neurological disorders, including schizophrenia, ADHDADD (attention deficit disorders), and neuronal disorders such as Alzaheimer's disease, Parkinson's disease, migraine and senile dementia. Additional disorders include inflammatory conditions (e.g. crohn's crospiratory allments such as asthma, and inflammatory diseases e.g.
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                                                                                                                                                                                                                                                                                                                                           New G protein-coupled receptor (nGPCR-x) and its encoding polynucleotide useful for diagnosing and treating e.g. schizophrenia
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                                                                                                                                                                                                                                                                                                                                                                                    Claim 4; Page 89; 261pp; English.
                                                                                                                                                                                                                                  (PHAA ) PHARMACIA & UPJOHN CO
                                                                                         2000US-0186530.
2000US-0186811.
2000US-0188114.
                                                                                                                                 2000US-0190310.
2000US-0190800.
2000US-0198568.
2000US-0201190.
                                                   2000US-0184129.
2000US-0185421.
2000US-0185554.
99US-0165838.
99US-0166071.
99US-0166678.
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25-MAY-2000; Z000US-0207094.
                                      99US-0173396
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Matches 1041; Conservative
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Schellin KA, Kaytes
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03-MAR-2000;
09-MAR-2000;
                                                                 28-FEB-2000;
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21-MAR-2000;
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02-MAY-2000;
                                                      22-FEB-2000;
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Human; GCPR; G-coupled protein-receptor; cardiant; antiarteriosclerotic; anabolic; cytostatic; antiviral; gene therapy; cardiomyopathy; obesity; anorexia; diabetes; osteoporosis; Crohn's disease; multiple sclerosis; asthma; Alzheimer's disease; Parkinson's disorder; Huntington's disease; infection; human immunodeficiency virus; HIV; ds.
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  241 TGGGCTTTTTGGGGACATTCCCTGCCGAGTGGGGCTCTTCACGTTGGCCATGAACAGGGCC
                                                           361 CACCACGCGGTGAACACTATCTCCACCCGGGTGGCGGCTGGCATCGTCTGCACCCTGTGG
                                                                                                                                                                                               GCCCTGGTCATCCTGGGAACAGTGTATCTTTGCTGGAGAACCATCTCTGCGTGCAAGAG
                                                                                                                                                                                                                                                                               541 TICCAGCIGGAGTICTTIAIGCCCCTCGGCAICAICTIAITITGCTCCTTCAAGAITGIT
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New human G-protein coupled receptor X, GPCRX, polypeptide useful in treatment or prevention of GPCRX associated disorders e.g. cardiomyopathy or atherosclerosis, and to screen for antagonists and adonists useful therapeutically
                                                                                                                                                                                                         agonists useful therapeutically
                                                                                                                                                                                                                   Claim 9; Page 7; 157pp; English.
             WO200174904-A2
                                               05-APR-2000; 2
06-APR-2000; 2
06-APR-2000; 2
06-APR-2000; 2
06-APR-2000; 2
06-APR-2000; 2
                                                                                            27-JUL-2000;
28-JUL-2000;
    Homo sapiens
                                           31-MAR-2000;
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Spytek KA,
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Mishnu VS, Tchernev VT,
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2000US-195069P.
2000US-195070P.
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11-OCT-2000; 2000US-239613P.
18-JAN-2001; 2001US-262508P.
23-JAN-2001; 2001US-263433P.
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2000US-219855P.
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30-MAR-2001; 2001WO-US10241
                                                                                     2000US-195066P
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The invention relates to nucleic acid sequences (ABAB1529-ABAB1552) that encode G-coupled protein-receptor related polypeptides

C (ABB4522-ABB4643). The isolated polypeptides

C (CPCRX) polypeptides. The polypeptides have potential cardiant.

C (CPCRX) polypeptides. The polypeptides have potential cardiant.

C (CPCRX) polypeptides. The polypeptides have potential cardiant.

C (CPCRX) polypeptides. The polypeptides have potential activity. The polypeptides can be administered therapeutically, especially using gene therapy and expressing the encoding DNA in vivo, to treat or prevent C GPCRX-associated disorders, especially in humans. For example, they can be used to treat/prevent cardiomyopathy, atheroscierosis, disorders cobssity, anorexia), diabetes, osteoporosis, Crohn's disease, multiple cobssity, anorexia), diabetes, osteoporosis, Crohn's disease, multiple cobssity, anorexia, disorders, neurodegenerative disorders, developmental diseases, neurological disorders, developmental diseases, neurological disorders, bacterial, fungal, protozoal and viral infections (e.g. with human communication and protocoal and viral infections (e.g. with human communication and protocoal and viral infections (e.g. with human communication and propeptide expression levels relative to detecting alterations in polypeptide expression levels relative to control samples. They are useful to identify agents binding polypeptide (e.g. cellular receptors or downstream effectors) and/or agents

C anticol and allored and a antagonists and agonists in disease treatment.

g

Sequence 1050 BP; 211 A; 299 C; 279 G; 261 T; 0 other;

305 365 420 425 485 540 545 605 9 720 725 845 61 CTGCTCATTGTGGCCTTTGTGCTGGGCGCACTAGGCAATGGGGTCGCCCTGTGTGTTTC 120 Gaps 9 65 186 GATITCCTCCTIATGATCTGCCTGCCTTTTCGGACAGACTATTACCTCAGACGTAGACAC 246 TGGGCTTTTGGGGACATTCCCTGCCGAGTGGGGCTCTTCACGTTGGCCATGAACAGGGCC 66 CIGCICALIGIGGCCITIGIGCIGGCGCACIAGGCAAIGGGGTCGCCCTGIGTGGTTTC GCCCTGGTCATCCTGGGAACAGTGTATCTTTTGCTGGAGAACCATCTCTGCGTGCAAGAG TGGAGCCTGAGGCGGAGCCAGCAGCTGGCCAGGCTCGGATGAAGAAGGCGACCCGG TTCATCATGGTGGTGGTGTTGTGTTCATCATGCTACCTGCCCAGCGTGTCTGCTAGA CTCTATTTCCTCTGGACGGTGCCTCGAGTGCCTGCGATCCCTCTGTCCATGGGGCCCTG CAGCCAGGACACTCAAAAACACAAAAGGCCGGAAGAGATGCCAATTTCGAACCTCGGTCGC AGGAGTTGCATCAGTGTGGCAAATAGTTTCCAAAGCCAGTCTGATGGGCAATGGGATCCC 1 ATGTACAACGGGTCGTGCTGCCGCATCGAGGGGGACACCATCTCCCCAGGTGATGCCGCCG TGCTTCCACATGAAGACCTGGAAGCCCAGCACTGTTTACCTTTTCAATTTGGCCGTGGCT GATTTCCTCCTTATGATCTGCCTGCCTTTTCGGACAGACTATTACCTCAGACGTAGACAC TGGGCTTTTGGGGACATTCCCTGCCGAGTGGGGCTCTTCACGTTGGCCATGACAGGGCC GGGAGCATCGTGTTCCTTACGGTGGTGGCTGCGGACAGGTATTTCAAAGTGGTCCACCCC CACCACGCGGTGAACACTATCTCCACCCGGGTGGCGGCTGGCATCGTCTGTGGCTGTGG GCCCTGGTCATCCTGGGAACAGTGTATCTTTTGCTGGAGAACCATCTCTGCGTGCAAGAG TGGAGCCTGAGGCGGAGCCAGCAGCTGGCCAGGCTCGGATGAAGAAGGCGACCCGG CACATAACCCTCAGCTTCACCTACATGAACAGCATGCTGGATCCCCTGGTGTATTTTT TCAAGCCCCTCCTTTCCCAAATTCTACAACAAGCTCAAAATCTGCAGTCTGAAACCCAAG Length 1050; ö Indels 22; ô 8 Score 1041; Pred. No. 0; Mismatches ; 100.0%; Conservative Similarity Best Local Sim Matches 1041; Query Match 9 301 361 486 909 999 984 841 901 196 306 366 421 126 481 541 546 601 199 721 726 781 846 ð g ò 8 à g ò g ò g ò g ò g à a ò a ò g ŏ g ð 8 ò g ò Q ò a ò g à

especially using gene

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polypeptides can be administered therapeutically,
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                                                                                                                                                                              anabolic; cytostatic; antiviral; gene therapy; cardiomyopathy; obesity; anorexia; diabetes; osteoporosis; Crohn's disease; multiple sclerosis; asthma; Alzhelmer's disease; Parkinson's disorder; Huntington's disease; infection; human immunodeficiency virus; HIV; ds.
                                                                                                                                                                       antiarteriosclerotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New human G-protein coupled receptor X, GPCRX, polypeptide useful in treatment or prevention of GPCRX associated disorders e.g. cardiomyopathy or atherosclerosis, and to screen for antagonists and
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Li L;
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Spytek KA,
                                                                                                                                                                       GCPR; G-coupled protein-receptor;
                                                                                                                                                 Human GPCR1b polynucleotide SEQ ID NO 3.
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Padigaru M, Mishnu VS, Tchernev VT,
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            1026 CACATTGTTGAGTGGCACTGA 1046
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 1021 CACATTGTTGAGTGGCACTGA 1041
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2000015-19510P-
2000015-21284P-
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2000015-2256P-
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P-PSDB; ABB44522.
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therapy and expressing the encoding DNA in vivo, to treat or prevent CC CPCRX-associated disorders, especially in humans. For example, they can be used to treat,prevent cardiomyopathy, atherosclerosis, disorders related to signal processing and metabolic pathway modulation (e.g. related to signal processing and metabolic pathway modulation (e.g. obesity, anorexia), diabetes, osteoporosis, Crohn's disease, multiple sclerosis, asthma, cancers, neurodegenerative disorders, immune disorders, disease, parkinson's disorders, immune disorders, bacterial, fungal, protozoal and viral infections (e.g. with human immunodeficiency virus (HIV)-1 or HIV-2). They can be used diagnostically to detecting alterations in polypeptide in mammals (especially humans) by detecting alterations in polypeptide in mammals (especially humans) by detecting alterations or downstream effectors) and/or agents modulating callular receptors or downstream effectors) and/or agents modulating callular polypeptide expression or activity, useful as antagonists in disease treatment.
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                                            CAGCCAGGACACTCAAAAACACAAAAGGCCGGAAGAGATGCCAATTTCGAACCTCGGTCGC
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Au-Young J;
                                  CACATAACCCTCAGCTTCACCTACATGAACAGCATGCTGGATCCCCTGGTGTATTTTT
                                                                                                                                                                                                                                                                                                                      Human; G-protein coupled receptor 3; cell proliferative disorder
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/product= "Human GCREC-3 protein"
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Khan FA, Gandhi
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25-MAY-2000;
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Elliott VS,
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The invention relates to human G-protein coupled receptor (GCREC)

polypeptides and polynucleotides. GCREC polypeptides are useful in

screening compounds that modulate their activity. They are useful in

the diagnosis, prevention and treatment of disorders which include

cell proliferative disorders such as arteriosclerosis, hepatitis,

myelofibrosis, psoriasis and cancer including adenocarchoma, leukaemia,

lymphoma; neurological disorders such as epilepsy, ischaemic

cerebrovascular disease, Alzheimer's disease, Pick's disease, dementia,

parkinson's disease, ataxias, multiple sclerosis, bacterial and viral

meningitis, Creutzfeldt-Jakob disease, schizophrenic disorders, amnesia;

cardiovascular disorders such as arteriovenous fistula, atherosclerosis,

hypertension, vascular tumours, myocardial infarction, hypertensive

cardiovascular disorders such as dysphagia, peptic ossophagitis,

cardiovascular disorders such as dysphagia, peptic ossophagitis,

dastrointestinal disorders such as dysphagia, peptic ossophagitis,

constipation, acquired immune deficiency syndrome (AIDS), hepatic

constipation, acquired inmune deficiency and acquired in accordance and observing and active acquired in accordance as infection caused by viral agent classified as adenovaries, and and the appropriations and tanman in metabolic disorders such as and fection caused by viral agent classified as adenovaries, areavitures, bunyavirus, bunyavi
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Novel G-protein coupled receptors and polynucleotides useful for diagnosis, treatment and prevention of disorders of cell proliferation, neurological, cardiovascular, metabolic disorders and viral infections
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/note= "G-protein coupled receptor"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protozoacide; analgesic; cytostatic; neuroleptic; nootropic; analgesic; cytostatic; neuroleptic; nootropic; analgesic; cytostatic; neuroleptic; nootropic; anthere as this central nervous system disease; CNS disease; cardiovascular disease; hypotrension; hypertension; angina pectoris; myocardial infartion; urinary retention; osteoporosis; ulcer; asthma; inflammation; allergy; benign prostatic hypertrophy; multiple sclerosis; psychotic disorder; neurological disorder; dyskinesia; huntington's disease; Tourette's syndrome; anxiety; schizophrenia; manic depression; delirium; dementia; mental retardation; ss.
                                                                                                                                                                                                                                                                                                                                AGGAGTTGCATCAGTGTGCCAAATAGTTTCCAAAGCCAGTCTGATGGGCAATGGGATCCC 1020
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HM74-11ke GPCR; G-protein coupled receptor; antibacterial; fungicide;
       TTCCAGCTGGAGTTCTTTATGCCCCTCGGCATCATCTTATTTTGCTCCTTCAAGATTGTT
                                                                                                                                                                                      CTCTATTTCCTCTGGACGGTGCCCTCGAGTGCCTGCGATCCCTCTGTCCATGGGGCCCTG
                                                                                                                                                                                                                                                           TCAAGCCCCTCCTTTCCCAAATTCTACAACAAGCTCAAAATCTGCAGTCTGAAACCCAAG
                                                                                                                                                                                                                                                                                              CAGCCAGGACACTCAAAAACACAAAGGCCGGAAGAGATGCCAATTTCGAACCTCGGTCGC
                                                                                               TTCCAGCTGGAGTTCTTTATGCCCCTCGGCATCATCTTATTTTTGCTCCTTCAAGATTGTT
                                                                                                                TGGAGCCTGAGGCGGAGCCAGCAGCTGGCCAGGCTCGGATGAAGAAGGCGACCCGG
                                                                                                                                                  TTCATCATGGTGGTGGTGTTGTGTTCATCATGCTACCTGCCCAGCGTGTCTGCTAGA
                                                                                                                                                                                                                        CACATAACCCTCAGCTTCACCTACATGAACAGCATGCTGGATCCCCTGGTGTATTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA encoding HM74-like G-protein coupled receptor (GPCR).
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The invention describes a novel isolated polynucleotide (I) encoding a human HM74-like GPCR are useful for modulating the activity of that regulate HM74-like GPCR are useful for modulating the activity of the regulate HM74-like GPCR are useful for modulating the activity of the protein in a disease selected from bacterial, fungal, protozoan, and (C) issase, cardiovascular disease, hypotension, publication, allowed from bacterial asthma, central nervous system (CNS) disease, cardiovascular disease, hypotension, hypotension, angina pectoris, myocardial infarction, urinary retention, osteoporosis, culcar, asthma, inflammation, allergy, benign prostatic hypertrophy.

CC ulcar, asthma, inflammation, allergy, benign prostatic hypertrophy, comittiple sclerosis and dyskinesia such as Huntington's disease and Tourette's syndrome. The composition is also useful for treating cortic and neurological disorders such as anxiety, schizophrenta, manic depression, delirium, dementia and severe mental retardation. (I) corticated diseases. (I) is useful in a diagnostic assay for detecting diseases, susceptibility to diseases and abnormalities related to the core and the core of mutations in the nucleic acid sequences which may act as agonists or antagonists at the receptor site and which can be regulated to provide therapeutic effects. The polypeptide is also useful as a bait corticum in a two-hybrid or three-hybrid assay, and to immunise a mammal cortic production of polyclonal antibodies. This sequence encodes the human cortical corti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel isolated polynucleotide, useful for treating infection, pain, cancer, asthma, hypertension, myocardial infarction, urinary retention, osteoporosis, encodes the human HM74-like G-protein coupled receptor
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100.0%; Score 1041; DB 24; Length 1730;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1041; Conservative 0; Mismatches 0; Indels 0;
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                                                                                           05-APR-2000; 2000US-194701P
04-APR-2001; 2001WO-EP03811
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/\*tag= a /product= "HM74-like\_GPCR"

Location/Qualifiers 464..1504

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                             CACCACGCGGTGAACACTATCTCCACCCGGGTGGCGGCTGGCATCGTCGTGCGCTGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gene encoding novel human G protein-coupled receptor (GPCR).
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The present invention relates to the isolation of a novel human G-protein coupled receptor (GPCR) which is related to the chemokine receptor coupled receptor (GPCR) which is related to the chemokine receptor (GPCR) which and gene sequences encoding for GPCR are also given in the invention. The sequences of the invention are useful conditions and treating diseases or conditions mediated by human proteases. Such diseases include hyperproliferative disorders (e.g. Parkinson's disease), ce.g. whyperplastal, neurological disorders (e.g. Parkinson's disease), ce.g. chizophrenia), inflammatory disorders (e.g. adult respiratory disorders (e.g. distress syndrome, ARDS). The GPCR protein is also useful for identifying a modulator of the expression of the protein. It also serves as a target or identifying agents for use in mammalian therapeutic applications, ce.g. a human drug, particularly modulating a biological or pathological response in a cell or tissue that expresses the protein, in biological assays related to GPCRs that are related to members of the chemokine receptor subfamily, in drug screening assays and in competition binding assays. GPCR is also useful in diagnosing a disease or predisobsition to a disease mediated by the peptide, in pharmacogenomic analysis. The polynucleotide sequences can also be used in gene therapy. The present contract of the numan GPCR gene sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                              Novel human G-protein coupled receptor proteins and nucleic acid molecules encoding the protein for use in developing human therapeutics and diagnostic compositions and for identifying modulators of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           490
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                                                                                                                                                                                                                                                                                        Di Francesco V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 23; Fig 3; 66pp; English.
                                                                   2000US-192419P.
2000US-230459P.
2000US-0666535.
27-MAR-2001; 2001WO-US09522
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                                                                   27-MAR-2000;
06-SEP-2000;
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GCPR; G-coupled protein-receptor; cardiant; antiarteriosclerotic;
                                                                                                                                                                                                                                                                                                                                                                                         anabolic; cytostatic; antiviral; gene therapy; cardiomyopathy; obesity; anorexia; diabetes; osteoporosis; Crohn's disease; multiple sclerosis; asthma; Alzhelmer's disease; Parkinson's disorder; Huntington's disease; infection; human immunodeficiency virus; HIV; ds.
                                                                                                                        AGGAGTTGCATCAGTGTGGCAAATAGTTTCCAAAGCCAGTCTGATGGGCAATGGGATCCC 1020
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            GCCCTGGTCATCCTGGGAACAGTGTATCTTTTGCTGGAGAACCATCTCTGCGTGCAAGAG
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                                                                                                                                                                                                TCAAGCCCCTCCTTTCCCAAATTCTACAACAAGCTCAAAATCTGCAGTCTGAAACCCAAG
                                                                                                                                                                                                                          CAGCCAGGACACTCAAAAACACAAAAGGCCGGAAGAAGATGCCAATTTCGAACCTCGGTCGC
                                 TTCCAGCTGGAGTTCTTTATGCCCCTCGGCATCATCTTATTTTGCTCCTTCAAGATTGTT
                                                                                      TGGAGCCTGAGGCGGAGCCAGCAGCTGGCCAGGCTCGGATGAAGAAGGCGACCCGG
                                                                                                                                                                     CACATAACCCTCAGCTTCACCTACATGAACAGCATGCTGGATCCCCTGGTGTATTATTTT
                                                                                                                                                                                                                                                                                                                                                                     Human GPCR1c polynucleotide SEQ ID NO 4.
                                                                                                                                                                                                                                                                                      CACATTGTTGAGTGGCACTGA 1351
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                                                                                                                                                                                                                                                                               CACATTGTTGAGTGGCACTGA 1041
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The invention relates to nucleic acid sequences (ABAB1529-ABAB152) that encode G-coupled protein-receptor related polypeptides having a sequence differing to the soluted polypeptide having a sequence differing by no more than 15 % of amino acid residues from one of 22 amino acid sequences (or mature forms of the sequences), fully defined in the sequences (or mature forms of the sequences), fully defined in the complete receptor X (GPCRX) polypeptides. The polypeptides have potential cardiant, antiarteriosclerotic, anabolic, cytostatic and antivital activity. The polypeptides can be administered therapeutically, especially using gene therapy and expressing the encoding DNA in vivo, to treat or prevent credited disorders, especially in humans. For example, they can be used to treat/prevent cardiomyopathy, atherosclerosis, disorders callomyopathy, atherosclerosis, disorders of chesity, anorexia) diabetes, osteoporosis, Crohn's disease, multiple sclerosis, asthma, cancers, neurodegenerative disorders, macropoietic disorders, developmental diseases, neurological disorders, bacentopoietic disorders, developmental diseases, neurological disorders, confremine the presence of or predisposition to a disease associated with altered levels of the polypeptide expression levels relative to control samples. They are useful to identify appears of the polypeptide expression levels relative to control samples. They are useful to identify appears of the polypeptide expression levels called to control samples.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New human G-protein coupled receptor X, GPCRX, polypeptide useful in treatment or prevention of GPCRX associated disorders e.g. cardiomyopathy or atherosclerosis, and to screen for antagonists and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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L1 L;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wolenc AR,
Spytek KA,
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Tchernev VT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 9; Page 11; 157pp; English.
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06-APR-2000; 2000US-195066P.
06-APR-2000; 2000US-195067P.
06-APR-2000; 2000US-195068P.
06-APR-2000; 2000US-195070P.
06-APR-2000; 2000US-195070P.
21-JUL-2000; 2000US-221284P.
27-JUL-2000; 2000US-221384P.
28-JUL-2000; 2000US-22458BP.
11-AUG-2000; 2000US-22458BP.
11-OCT-2000; 2000US-22458BP.
11-AUG-2000; 2000US-22458BP.
11-AUG-2000; 2000US-22458BP.
11-AN-2001; 2001US-26550BP.
23-JAN-2001; 2001US-26550BP.
23-JAN-2001; 2001US-26550BP.
29-JAN-2001; 2001US-26550BP.
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P-PSDB; ABB44523.
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Padigaru M,
Baumgartner J
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2000US-193664P.

2000US-194614P

31-MAR-2000; 2 05-APR-2000; 2 06-APR-2000; 2

30-MAR-2001; 2001WO-US10241.

11-OCT-2001.

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          GCCCTGGTCATCCTGGGAACAGTGTATCTTTTGCTGGAGAACCATCTCTGCGTGCAAGAG
                                                                                                                                                                                                                                      TICCAGCIGGAGTICTITATGCCCCTCGGCATCATCTTATTTTGCTCCTTCAAGATTGTT
                                                                                                                                                                                                                                                                                                                     TGGAGCCTGAGGCGGAGCCAGCTGGCCAGCCAGGCTCGGATGAAGAAGGCGACCCGG
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 TGCTTCCACATGAAGACCTGGAAGCCCAGCACTGTTTACCTTTTCAATTTGGCCGTGGCT
                                                                             TGGGCTTTTGGGGACATTCCCTGCCGAGTGGGGGCTCTTCACGTTGGCCCATGAACAGGGCC
                                                                                               TGGGCTTTTGGGGACATTCCCTGCCGAGTGGGGCCTCTTCACGTTGGCCCATGAACAGGGCC
                                                                                                                  GGGAGCATCGTGTTCCTTACGGTGGTGGCTGCGGACAGGTATTTCAAAGTGGTCCACCCC
                                                                                                                                                         CACCACGCGGTGAACACTATCTCCACCCGGGTGGCGGCTGGCATCGTTGCACCCTGTGG
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DNA; 888

AAH50974 standard;

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RESULT 10 AAH50974 AAH50974;

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28-AUG-2001 (first entry)

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The present invention relates to novel G protein-coupled receptors

(nGPCRx; where x is 1, 3, 4, 5, 9, 11, 12, 14-18, 20, 21, 22, 24, 27,

28, 31-38, 40, 41, 53-60) and their coding sequences. The present

sequence is the coding sequence for one such G protein-coupled receptor.

GPCRs are also known as seven transmembrane receptors and function in

signal transduction. The nGPCRx coding sequences are useful for

signal transduction, apecifically schizophrenia. nGPCRx are useful for

creening a human to diagnose a disorder affecting the brain or a genetic

predisposition, specifically schizophrenia. nGPCRx are useful for

conferex in a sample is useful for treating schizophrenia. Detection of

disorders e.g. thyroid disorders, renal failure, rheumatoid arthritis,

CNS disorders, infections such as HIV-1, metabolic and cardiovascular

disorders, infections such as HIV-1, metabolic and cardiovascular

disorders, infections such as HIV-1, metabolic and cardiovascular

chiseases, proliferative disorders and hormonal disorders, modulators of

nGPCRx activity have the utility for treating neurological disorders,

including schizophrenia, ADHD/ADD (attention deficit-hyperactivity

disorder/attention deficit disorder), and neuronal disorders such as

Alzheimmer's disease, parkinson's disease, migraine and semile dementia.

Additional disorders include inflammatory conditions (e.g. Crohn's

disease), rheumatoid arthritis, autoimmune disorders, cancers,

conditional disorders and hormonal disorders, cancers,

conditional disorders and hormonal disorders e.g.
                                                                     signal transduction; schizophrenia; thyroid disorder; renal failure; rheumatoid arthritis; CNS disorder; infection; metabolic disease; cardiovascular disease; proliferative disorder; hormonal disorder; neurological disorder; neuronal disorder; Alzheimer's disease; cancer; attention deficit thyperactivity disorder/attention deficit disorder; parkinson's disease; migraine; senile dementia; inflammatory disease; rheumatoid arthritis; autoimmune disorder; respiratory ailment;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New G protein-coupled receptor (nGPCR-x) and its encoding polynucleotide useful for diagnosing and treating e.g. schizophrenia
                                                       receptor;
enal failure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nd P, Slightom J;
Sejlitz T, Huff
                                                       seven transmembrane
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an CM, Ruff
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               Human nGPCR11 coding sequence #1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (PHAA ) PHARMACIA & UPJOHN CO.
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2000US-0185554.
2000US-0186530.
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99US-0166678.
99US-0173396.
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                                                       protein-coupled receptor;
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                                                                                                                                                                                                          neuroprotective; ds
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02-MAR-2000;
03-MAR-2000;
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17-MAR-2000;
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19-NOV-1999;
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hRUP25. The endogenous and non-endogenous, constitutively activated versions of human G-protein coupled receptors (GPCR), are useful for direct identification of candidate compounds as receptor agonists, inverse agonists or partial agonists having applicability as therapeutic agents for treating diseases related to GPCR, e.g. lung cancer. Non-endogenous version of human GPCRs are also utilized in research settings and in vitro and in vivo system, incorporating GPCRs can be utilised to elucidate and understand the roles these receptors play in the human condition, both normal and diseased.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Endogenous and non-endogenous versions of human G-protein coupled receptors for direct identification of candidate compounds as agonists, inverse agonists or partial agonists for use as therapeutic agents -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence encodes a human G-protein coupled receptor (GPCR)
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                                                                                        Human; G-protein coupled receptor; GPCR; hRUP25; agonist;
inverse agonist; lung cancer; ss.
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                                               encoding G-protein coupled receptor,
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2000US-0203630.
2000US-0210741.
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20000S-0235779.
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99US-0166369
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2000US-0189258
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2000US-0226760
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P-PSDB; AAU04379.
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14-MAR-2000;
10-APR-2000;
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12-MAY-2000;
12-JUN-2000;
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26-SEP-2000;
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  23-OCT-2001
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                                               Length
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Sequence 888 BP; 174 A; 254 C; 231 G; 229 T; 0 other;
                                                                                          ö
                                             DB 22;
                                        85.3%; Score 888; DB
100.0%; Pred. No. 0;
ive 0; Mismatches
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                                                                                             Conservative
                                          Query Match
Best Local Similarity
Matches 888; Conserv
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us-09-886-041-1.olig.rng

790 CTCAGCTTCACCTACATGAACAGCATGCTGGA 821

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The invention relates to constitutively active, non-endogenous versions of endogenous human orphan G protein-coupled receptors (GPCRS, AAY90643-AAY90677 and AAA30779-A397743 and treamanness of them (AAA30779-A30779). The mutant proteins of the invention contain a mutation in a portion of the protein comprising intracellular loop 3 (TS) and transmembrane domain 6 (TM6). A non-endogenous annino acid, X, as substituted for an endogenous residue in IC3 at a position 16 amino acids N-terminal of an endogenous proline in TM6 to form a sequence X(AA)15-Pror. The endogenous amino acid is selected from Lys, His, Arg or Ala, and is preferably Lys. When the endogenous residue at this position is Lys, this residue is replaced by His, Arg or preferably Ala. The Lib amino acid stretch between the substituted amino acid and the Promonendogenous, non-endogenous, or a mixture of endogenous and the Promonendogenous residues. The constitutively active GPCRs are useful for dentifying antagonists, agonists and partial agonists for elucidating the roles of the receptors in normal and settings for elucidating the roles of the receptors in normal and setting for elucidating the roles of the receptors in normal and disorders associated with that receptor. Because the novel mutant GPCRs are constitutively active, they can be used disorders associated with the need for endogenous constitutively active, they can be used directed may be present sequence represent cDNA encoding a human wild-type GPCR used in an exemplification of the invention. This was cloned and subsequence the constitutively active, they can be used and present and present and present sequence represents cDNA encoding a human wild-type the constitution of the invention of the invention of the constitution of the invention of the constitution of the consti
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  G protein-coupled receptor; GPCR; constitutively active; intracellular loop 3; transmembrane domain 6; drug screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1164 BP; 246 A; 337 C; 288 G; 293 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human G protein-coupled receptor HM74 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the corresponding mutant of the invention.
Example 1; Page 185; 341pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Behan DP, Chalmers DT, Liaw CW;
                                                                                                                                                                                                                                                                                               AAA30658 standard; cDNA; 1164 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99WO-US23938.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                agonist; antagonist; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (AREN-) ARENA PHARM INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                  AAA30658;
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                                                                                                                                                                                                      RESULT 12
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The invention relates to constitutively active, non-endogenous versions of endogenous human orphan G protein-coupled receptors (GPCRs, AAY90643-AAY90677 and AAAY90677 and AAAY90677 and AAAY90677 and AAAY9079). The mutant proteins of the invention contain a mutation in a portion of the protein comprising intracellular loop 3 (TS3) and transmembrane domain 6 (TM6). A non-endogenous amino acid, x, is substituted for an endogenous proline in IC3 at a position 16 amino acids N-terminal of an endogenous proline in TM6 to form a sequence X (AAA)13-pro. The endogenous amino acid is selected from Lys, His, Arg or Ala, and is preferably Lys. When the endogenous residue at this position is Lys, this residue is replaced by His, Arg or preferably Ala. The IS amino acid stretch between the substituted and the Promay be endogenous, non-endogenous, or a mixture of endogenous and non-endogenous. The constitutively active GPCRs are useful for identifying antagonists, agonists and partial agonists for use as electing for elucidating the roles of the receptors in normal and settings for elucidating the roles of the receptors in normal and conservations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for screening of compounds without the need for endogenous
Sequences AAA30709- AAA30743 and AAA30775-A30779 represent DNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       treating diseases and disorders associated with that receptor. Because the novel mutant GPCRs are constitutively active, they can be used
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Non-endogenous constitutively activated human G protein-coupled receptors, useful for identifying agonists for use as pharmaceutical
                                                                                                                                                                                                                                                    DNA encoding human mutant G protein-coupled receptor HM74 (1230K).
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                                                                                                                                                                                                                                                                                            G protein-coupled receptor; GPCR; constitutively active; intracellular loop 3; transmembrane domain 6; drug screening;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          encoding the mutant human GPCRs of the invention.
838 CTCAGCTTCACCTACATGAACAGCATGCTGGA 869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 2; Page 285-286; 341pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Liaw CW;
                                                                                                                                                                                                                                                                                                                 intracellular loop 3; transmembr
agonist; antagonist; mutant; ss.
                                                                                                                        AAA30738 standard; DNA; 1164 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98US-0170496
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Behan DP, Chalmers DT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (AREN-) ARENA PHARM INC
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                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                 AAA30738;
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                                                                                   RESULT 13
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Gaps

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3.1%; Score 32; DB 21; Length 1164; 100.0%; Pred. No. 8.9e-06; Live 0; Mismatches 0; Indels C

Query Match Best Local Similarity 100.0 Matches 32; Conservative

AAH51053 standard; DNA; 24 BP.

RESULT 15 AAH51053 Oligonucleotide SEQ ID 133.

(first entry)

28-AUG-2001

AAH51053;

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The present sequence encodes a member of the G-protein coupled receptor additions, and receptor) family, designated the HM74A receptor. The proteins, agonists, antagonists and polynucleotides can be used for treating disorders associated with increased or reduced expression or activity of HM74A, e.g. bacterial, fungal, protozoan and viral infections, particularly infections caused by HHV-1 or HIV-2, pain, cancers, diabetes, obesity, anorexia, bulimia, asthma, Parkinson's disease, acute heart failure, hypotension, hypertension, urinary retention, osteoporosis, angina pectoris, myocardial infarction, stroke, ulcers, asthma, allergies, benign prostatic hypertrophy, migraine, vomiting, psychotic and neurological disorders, including anxiety, schizophrenia, mand depression, delirium, dementia, and severe mental retardation, and dyskinesias such as Huntington's disease or clines de la Tourett's syndrome. The products can also be used for detection, diagnosis and drug screening.
                                                                                                                                                                                                                                                      HM74A receptor; G-protein coupled receptor; infection; pain; cancer; diabetes; obesity; neurological disorder; heart failure; hypertension;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated G-protein coupled receptor, HM74A - used to develop products for treating e.g. infections, pain, cancers, diabetes, obesity, neurological disorders, heart failure, hypertension, asthma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mooney JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1361 BP; 291 A; 390 C; 342 G; 338 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Li X,
                                                                                                                                                                                                                       G-protein coupled receptor HM74A encoding cDNA
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100.0%; Pred. No. co.
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                         /*tag= a
/product= "HM74A receptor"
                 CTCAGCTTCACCTACATGAACAGCATGCTGGA 821
                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 2; Page 30-31; 40pp; English.
                                                                                                                   AAX16671 standard; cDNA; 1361 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SMIK ) SMITHKLINE BEECHAM CORP.
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                                                                                                                                                                                     29-APR-1999 (first entry)
                                                                                                                                                                                                                                                                                       asthma; allergy; ss.
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                                                                                                                                                                                                                                                                                                                          Homo sapiens
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                                                                                                                                                    AAX16671;
190
                                 838
                                                                                   RESULT 14
                                                                                                                                                                                                                                                                                                                                                          Key
                                                                                                   AAX1667.
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The present invention relates to novel G protein-coupled receptors (nGPCRx; where x 1s 1, 3, 4, 5, 9, 11, 12, 14-18, 20, 21, 22, 24, 27, 28, 31-38, 40, 41, 51-60) and their coding sequences (see AAH51015 and AAH51010S and AAG80929-AAG80975 and AAG80977). The present sequence is an oligonucleotide, which was used in the present invention. GPCRs are also known as seven transmembrane receptors and thurshin in signal transduction. The nGPCRx coding sequences are useful for screening a human to diagnose a disorder affecting the brain or a genetic predisposition, specifically schizophrenia. nGPCRx are useful for identifying compounds useful for treating schizophrenia. Detection of GPCRx in a sample is useful as a diagnostic tool for diseases or disorders e.g. thyroid disorders, renal failure, rheumatoid arthritis, CNS disorders, infections such as HIV-1, metabolic and cardiovascular diseases, proliferative disorders and hormonal disorders. Modulators of
                                                                                                              G protein-coupled receptor; nGPCR; seven transmembrane receptor; signal transduction; schizophrenia; thyroid disorder; renal failure; rheumatoid arthritis; CNS disorder; infection; metabolic disease; cardiovascular disease; proliferative disorder; hormonal disorder; neurological disorder; neuronal disorder; Alzheimer's disease; cancer; attention deficit-hyperactivity disorder/attention deficit disorder; parkinson's disease; migraine; senile dementia; inflammatory disease; rheumatoid arthritis; autoimmune disorder; respiratory ailment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           di LA, Hiebsch RR, Lind P, Slightom J;
Bannigan CM, Ruff V, Sejlitz T, Huff RM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New G protein-coupled receptor (nGPCR-x) and its encoding polynucleotide useful for diagnosing and treating e.g. schizophrenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 246; 261pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Parodi LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (PHAA ) PHARMACIA & UPJOHN CO.
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2000US-0185554.
2000US-0186530.
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99US-0166678.
99US-0173396.
2000US-0184129.
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2000US-0201190
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                                                                                                                                                                                                                                                              neuroprotective; ss
                                                                                                                                                                                                                                                                                                                              WO200136473-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-FEB-2000; 2
28-FEB-2000; 2
02-MAR-2000; 2
03-MAR-2000; 2
09-MAR-2000; 2
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02-MAY-2000;
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22-FEB-2000;
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                                                                                                                                                                                                                                                                                              Synthetic.
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Gaps

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790 CTCAGCTTCACCTACATGAACAGCATGCTGGA 821

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Matches 32; Conservative

Local Similarity

Query Match

Length 1361; Indels

score 32; DB 20; I Pred. No. 8.9e-06;

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nGPCRx activity have the utility for treating neurological disorders, including schizophrenia, ADHD/ADD (attention deficit-hyperactivity disorder/attention deficit disorder) and neuronal disorders such as Alzheimer's disease, Parkinson's disease, migraine and senile dementia. Additional disorders include inflammatory conditions (e.g. Crohn's disease), rheumatoid arthritis, autoimmune disorders, cancers, respiratory aliments such as asthma, and inflammatory diseases e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                            G protein-coupled receptor; nGPCR; seven transmembrane receptor; signal transduction; schizophrenia; thyroid disorder; renal failure; rheumatoid arthritis; CNS disorder; infection; metabolic disease; cardiovascular disease; proliferative disorder; hormonal disorder; neurological disorder; neuronal disorder; Alzheimer's disease; cancer; attention deficit-hyperactivity disorder/attention deficit disorder; Perkinson's disease; migraine; senile dementia; inflammatory disease; rheumatoid arthritis; autoimmune disorder; respiratory ailment; neuroprotective; PCR primer; ss.
                                                                                                                                                                                               Gaps
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                                                                                                                                                             Score 24; DB 22; Length 24;
Pred. No. 0.094;
0; Mismatches 0; Indels
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                                                                                                                                   Sequence 24 BP; 3 A; 7 C; 5 G; 9 T; 0 other;
                                                                                                                                                                        100.08; Pred. NC.
                                                                                                                                                                                                                       707 GCGTGTCTGCTAGACTCTATTTCC 730
                                                                                                                                                                                                                                     1 GCGTGTCTGCTAGACTCTATTTCC 24
                                                                                                                                                                                                                                                                                                                                                                                                                  Human nGPCR11 PCR primer LW1660.
                                                                                                                                                                                                                                                                                                                           AAH51082 standard; DNA; 24 BP.
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99US-0166678.
99US-0173396.
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2000US-0186530.
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09-MAR-2000; 2000US-0188114.
17-MAR-2000; 2000US-0190310.
21-MAR-2000; 2000US-0190800.
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2000US-0201190.
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                                                                                                                                                                                                                                                                                                                                                                                     28-AUG-2001 (first entry)
                                                                                                                                                                           Local Similarity 100.
nes 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schellin KA, Kaytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wood LS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-389826/41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200136473-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-FEB-2000;
02-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-NOV-1999;
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28-DEC-1999
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                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                        AAH51082;
                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                               RESULT 16
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New G protein-coupled receptor (nGPCR-x) and its encoding

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                                                                                                                                                                                                                                          or agenetic predisposition, specifically schizophrenia, nGPCRx are useful for identifying compounds useful for treating schizophrenia. Detection of nGPCRx in a sample is useful for treating schizophrenia. Detection of nGPCRx in a sample is useful for treating schizophrenia. Detection of nGPCRx in a sample is useful for treating schizophrenia architis. CNS disorders, infections such as HIV-1, metabolic and architiss collaborators, proliferative disorders and hormonal disorders. Modulators of nGPCRx activity have the utility for treating neurological disorders, including schizophrenia, ADHD/ADD (attention deficit-hyperactivity disorderfy, and neuronal disorders such as Alzheimer's disease, Parkinson's disease, migraine and senile dementia. Additional disorders include inflammatory conditions
                                                                         The present invention relates to novel G protein-coupled receptors (nGPCRx; where x is 1, 3, 4, 5, 9, 11, 12, 14-18, 20, 21, 22, 24, 27, 28, 31-38, 40, 41, 53-60) and their coding sequences (see AAH50699-AAH51015 and AAH5105 and AAG80929-AAG80975 and AAG80977). The present sequence is a PCR primer, which was used in an example from the present invention. GPCRs are also known as seven transmembrane receptors and function in signal transduction. The nGPCRx coding sequences are useful for screening a human to diagnose a disorder affecting the brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (e.g. Crohn's disease), rheumatoid arthritis, autoimmune disorders, cancers, respiratory ailments such as asthma, and inflammatory diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     G protein-coupled receptor; nGPCR; seven transmembrane receptor; signal transduction; schizophrenia; hybroid disorder; renal failure; rhematoid arthritis; CNS disorder; infection; metabolic disease; cardiovascular disease; proliferative disorder; hormonal disorder; neuronal disorder; attention deficit-hyperacrivity disorder; Alzheimer's disease; cancer; attention deficit-hyperacrivity disorder/attention deficit disorder: Parkinson's disease; migraine; senile dementia; inflammatory disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
polynucleotide useful for diagnosing and treating e.g. schizophrenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rheumatoid arthritis; autoimmune disorder; respiratory ailment;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.3%; Score 24; DB 22; Length 24; 100.0%; Pred. No. 0.094; ve 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 24 BP; 3 A; 7 C; 5 G; 9 T; 0 other;
                                       Example 11; Page 143; 261pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          707 GCGTGTCTGCTAGACTCTATTTCC 730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     e.g. inflammatory bowel disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.08;
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990S-0166678.
990S-0173396.
20000S-018429.
20000S-0185421.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oligonucleotide SEQ ID 130.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               neuroprotective; ss
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28-FEB-2000;
28-FEB-2000;
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17-NOV-1999;
19-NOV-1999;
28-DEC-1999;
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Matches
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rheumatoid arthritis; autoimmune disorder; respiratory ailment;
            neuroprotective; PCR primer; ss
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                                                                                                                                                                                                                                                                                                                                                                                                              Wood
                                                                  WO200136473-A2
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Schellin KA,
                                         Homo sapiens.
                                                                                                                                                                                                                                                                                     17-MAR-2000;
21-MAR-2000;
                                                                                                                       16-NOV-2000;
                                                                                             25-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24;
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                     present sequence is an oligonucleotide, which was used in the present invention. GPCRs are also known as seven transmembrane receptors and invention in Signal transduction. The indeptx coding sequences are useful for screening a human to diagnose a disorder affecting the brain or a genetic predisposition, specifically schizophrenia. nGPCRx are useful for identifying compounds useful for treating schizophrenia. Detection of indeptx in a sample is useful as a diagnostic tool for diseases or infections such as HIV-1, metabolic and cardiovascular disorders, infections such as HIV-1, metabolic and cardiovascular clientivity have the utility for treating neurological disorders, including schizophrenia, ADHD/ADD (attention deficit-hyperactivity disorders lucing disorders such as the latentian deficit disorder), and neuronal disorders such as Additional disorders include inflammatory conditions (e.g. Crohn's disease), rheumatoid arthritis, autoimmune disorders, cancers, consers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                    The present invention relates to novel G protein-coupled receptors (nGPCRX; where x is 1, 3, 4, 5, 9, 11, 12, 14-18, 20, 21, 22, 24, 27, 28, 31-38, 40, 41, 53-60) and their coding sequences (see AAH50059-AAH51015 and AAH51105 and AAG80929-AAG80975 and AAG80977). The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       G protein-coupled receptor; nGPCR; seven transmembrane receptor; signal transduction; achizophrania; hypoid disorder; renal failure; rhematoid arthritis; CNS disorder; infection; metabolic disease; cardiovascular disease; proliferative disorder; hormonal disorder; neuronal disorder; attention deficit-hyperactivity disorder; Altchiun deficit disorder; attention deficit disorder; Parkinson's disease; cancer; Parkinson's disease; migraine; senile dementia; inflammatory disease;
                                                                                                                                                                od LS, Parodi LA, Hiebsch RR, Lind P, Slightom J;
Kaytes PS, Bannigan CM, Ruff V, Sejlitz T, Huff RM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                  New G protein-coupled receptor (nGPCR-x) and its encoding polynucleotide useful for diagnosing and treating e.g. schizophrenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          respiratory ailments such as asthma, and inflammatory diseases e.g.
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Pred. No. 0.093;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 52 BP; 12 A; 14 C; 12 G; 14 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 245; 261pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCGTGTCTGCTAGACTCTATTTCC 730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human nGPCR11 PCR primer LW1658.
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                                                                                                                                      (PHAA ) PHARMACIA & UPJOHN CO
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                                      2000US-0190310.
2000US-0190800.
2000US-0198568.
2000US-0201190.
                                                                                             08-MAY-2000; 2000US-0203111.
25-MAY-2000; 2000US-0207094.
            2000US-0186811
2000US-0188114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           inflammatory bowel disease.
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                                                                                                                                                                                                         WPI; 2001-389826/41.
                                                                                                                                                                 Wood LS,
                                      17-MAR-2000;
21-MAR-2000;
20-APR-2000;
02-MAY-2000;
                                                                                                                                                                Vogeli G, Woo
Schellin KA,
                            09-MAR-2000;
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Matches
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The present invention relates to novel G protein-coupled receptors (nGPCRx; where x is 1, 3, 4, 5, 9, 11, 12, 14-18, 20, 21, 22, 24, 27, 28, 31-38, 40, 41, 53-60) and their coding sequences (see 28, 31-38, 40, 41, 53-60) and their coding sequences (see AAH51015 and AAH51059-AAG80975 and AAG80977). The present sequence is a PCR primer, which was used in an example from the present invention GPCRs are also known as seven transmembrane receptors and function in signal transduction. The nGPCRx coding sequences are useful for screening a human to diagnose a disorder affecting the brain or a genetic predisposition, specifically schizophrenia. nGPCRx are useful for identifying compounds useful for treating schizophrenia.

Or a genetic predisposition, specifically schizophrenia chection of nGPCRx in a sample is useful as a diagnostic tool for diseases or disorders e.g. thyroid disorders, renal failure, rheumatoid arthitis, CNS disorders, prolifections such as HIV-1, metabolic and cardiovascular diseases, proliferative disorders and hormonal disorders. Modulators of nGPCRx activity have the utility for treating neurological disorders including schizophrenia, ADHD/ADD (attention deficit-flow hyperactivity disorder/attention deficit disorders, migraine and disorders such as Alzheimer's disease, Parkinson's disease, migraine and senile demential. Additional disorders includes and includers includes and includers includes and includers included emention deficit disorder includes and proper activity disorder. Additional disorders includes and disorders includes and disorders included inflammatory conditions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Slightom J;
rz T. Huff RM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New G protein-coupled receptor (nGPCR-x) and its encoding polynucleotide useful for diagnosing and treating e.g. schizophrenia
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Raytes PS, Bannigan CM, Ruff V, Sejlitz T,
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Pred. No. 0.093;
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100.0%; Pre-
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17-NOV-1999; 990S-0166671.

19-NOV-1999; 990S-0166678.

28-DEC-1999; 990S-0166678.

22-FEB-2000; 2000US-01854129.

28-FEB-2000; 2000US-0185421.

28-FEB-2000; 2000US-018554.

02-MAR-2000; 2000US-018554.

03-MAR-2000; 2000US-0186530.
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20-APR-2000; 2000US-0198568.
02-MAY-2000; 2000US-0201190.
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RESULT 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (nGPCRx; where x is 1, 3, 4, 5, 9, 11, 12, 14-18, 20, 21, 22, 24, 27, 28, 31-38, 40, 41, 53-60) and their coding sequences (see AAH51015 and AAH51105 and AAG80929-AAG80975 and AAG80977). The
                                                                                                                                                                                                                  signal transduction; schizophrenia; thyroid disorder; renal failure; rheumatoid arthritis; CNS disorder; infection; metabolic disease; cardiovascular disease; proliferative disorder; hormonal disorder; neurological disorder; neuronal disorder; hormonal disorder; attention deficit-hyperactivity disorder/attention deficit disorder; parkinson's disease; migralne; senile dementia; inflammatory disease; rheumatoid arthritis; autoimmune disorder; respiratory ailment; neuroprotective; PCR primer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New G protein-coupled receptor (nGPCR-x) and its encoding polynucleotide useful for diagnosing and treating e.g. schizophrenia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vogeli G, Wood LS, Parodi LA, Hiebsch RR, Lind P, Slightom J;
Schellin KA, Kaytes PS, Bannigan CM, Ruff V, Sejlitz T, Huff
                                                                                                                                                                                                  G protein-coupled receptor; nGPCR; seven transmembrane receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 2; Page 101; 261pp; English.
                                                                                                                                                               Human nGPCR11 PCR primer LW1565.
                                                  AAH51029 standard; DNA; 33 BP
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99US-0166678.
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2000US-0185421
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                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                               WO200136473-A2.
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22-FEB-2000;
28-FEB-2000;
28-FEB-2000;
02-MAR-2000;
03-MAR-2000;
07-MAR-2000;
17-MAR-2000;
21-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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08-MAY-2000;
                                                                                                                          28-AUG-2001
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                                                                                       AAH51029;
               RESULT 19
AAH51029/c
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disorders, including schizophrenia, ADHD/ADD (attention deficithyperactivity disorder/attention deficit disorder), and neuronal disorders such as Alzheimer's disease, Parkinson's disease, migraine and senile dementia. Additional disorders include inflammatory conditions (e.g. Crohn's disease), rheumatoid arthritis, autolumnue disorders, cancers, respiratory ailments such as asthma, and inflammatory diseases e.g. inflammatory bowel disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                signal transduction; schizophrenia; thyroid disorder; renal failure; rheumatoid arthritis; CNS disorder; infection; metabolic disease; cardiovascular disease; proliferative disorder; hormonal disorder; neurological disorder; neuronal disorder; Alzheimer's disease; attention deficit-hyperactivity disorder/attention deficit disorder; sparkinson's disease; migraine; senile dementia; inflammatory disease; rheumatoid arthritis; autoimmune disorder; respiratory ailment; neuroprotective; PCR primer; ss.
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PS, Bannigan CM, Ruff V, Sejlitz T, Huff RM;
                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                              DB 22; Length 33;
                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                    0.3;
                                                                                                                                                                                                                                 Sequence 33 BP; 9 A; 8 C; 8 G; 8 T; 0 other;
                                                                                                                                                                                                                                                                                                                                           1019 CCCACATTGTTGAGTGGCACTGA 1041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human nGPCR11 PCR primer LW1564.
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2000US-0185421.
2000US-018554.
2000US-0186530.
2000US-0186811.
2000US-0188114.
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2000US-0198568.
2000US-0201190.
2000US-0203111.
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99US-0166678.
99US-0173396.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAH51028 standard; DNA; 33
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                                                                                                                                                                                                                                              Query Match 2.2%
Best Local Similarity 100.(
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kaytes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200136473-A2.
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09-MAR-2000; 2
17-MAR-2000; 2
21-MAR-2000; 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-NOV-1999;
28-DEC-1999;
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02-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-APR-2000;
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                                     The present invention relates to novel G protein-coupled receptors

(nGPCRx; where x is 1, 3, 4, 5, 9, 11, 12, 14-18, 20, 21, 22, 24, 27,

28, 31-38, 40, 41, 53-60) and their coding sequences (see
ANH50869-AAH51015 and AAH5105 and AAG80929-AAG80975 and AAG80977). The
present sequence is a PCR primer, which was used in an example from the
present invention. GPCRs are also known as seven transmembrane receptors
and function in signal transduction. The nGPCRx coding sequences are
useful for screening a human to diagnose a disorder affecting the brain
cor a genetic predisposition, specifically schizophrenia. nGPCRx are
useful for identifying compounds useful for treating schizophrenia.

Cuseful for identifying compounds useful as a diagnostic tool for
diseases or disorders e.g. thyroid disorders, renal failure, rheumatoid
arthritis, CNS disorders, infections such as HIV1, metabolic and
cardiovascular diseases, proliferative disorders and hormonal disorders.

Modulators of nGPCRx activity have the utility for treating neurological
disorders, including schizophrenia, AHDA/DD (attention deficit.
hyperactivity disorder/attention deficit disorder, and neuronal
cardiovascular disease, proliferative disorder, and neuronal
disorders such as Alzheimer's disease, Parkinson's disease, migraine and
senie dementia. Additional disorders include inflammatory diseases
cancers, respiratory aliments such as asthma, and inflammatory diseases
e.g. inflammatory bowel disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        G protein-coupled receptor; nGPCR; seven transmembrane receptor; signal transduction; schizophrenia; thyroid disorder; renal failure; rheumatoid arthritis; CNS disorder; infection; metabolic disease; cardiovascular disease; proliferative disorder; hormonal disorder; neurological disorder; neuronal disorder; Alzheimer's disease; cancer; attention deficit. Thyperactivity disorder; Alzheimer's disease; cancer; Parkinson's disease; migralne; senile dementia; inflammatory disease; rheumatoid arthritis; autoimmune disorder; respiratory ailment; neuroprotective; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                                                                        2.0%; Score 21; DB 22; Length 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                       Sequence 33 BP; 7 A; 9 C; 9 G; 8 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                      red. No. 3;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No.
               Example 2; Page 101; 261pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                    2.00,
100.08; Pre-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ATGTACAACGGGTCGTGCTGC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13 ATGTACAACGGGTCGTGCTGC 33
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990S-0166671.
990S-0116678.
990S-0113396.
2000US-0184129.
2000US-018554.
2000US-0185554.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human nGPCR11 PCR primer #1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
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28-FEB-2000;
02-MAR-2000;
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28-DEC-1999;
22-FEB-2000;
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The present invention relates to novel G protein-coupled receptors (nGPCRx: where x is 1, 3, 4, 5, 9, 11, 12, 14-18, 20, 21, 22, 24, 27, 28, 31-38, 40, 41, 53-60) and their coding sequences (see 28, 31-38, 40, 34, 51-60) and their coding sequences (see present sequence is a PCR primer, which was used in an example from the present sequence is a PCR primer, which was used in an example from the present invention. GPCRs are also known as seven transmembrane receptors and function in signal transduction. The nGPCRx coding sequences are useful for screening a than an of diagnose a disorder affecting the brain or a genetic predisposition, specifically schizophrenia. nGPCRx are useful for identifying compounds useful for treating schizophrenia.

Or a genetic predisposition, specifically schizophrenia checking in a sample is useful as a diagnostic tool for diseases or disorders e.g. thyroid disorders, renal failure, rheumatoid arthitis, CRS disperders, infections such as HIV1, metabolic and cardiovascular diseases, proliferative disorders and hormonal disorders. Modulators of nGPCRx activity have the utility for treating neurological disorders, including schizophrenia, ADHD/ADD (attention deficit-disorders, understunders and alsorders and disorders 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (e.g. Crohn's disease), rheumatoid arthitis, autoimmune disorders, cancers, respiratory aliments such as asthma, and inflammatory diseases e.g. inflammatory bowel disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         G protein-coupled receptor; nGPCR; seven transmembrane receptor; signal transduction; schizophrenia; thyroid disorder; renal failure; rheumatoid arthritis; CNS disorder; infection; metabolic disease; cardiovascular disease; proliferative disorder; hormonal disorder; neurological disorder; neuronal disorder; Alzheimer's disease; cancer; attention defilict hyperactivity disorder/attention defilict disorder; Parkinson's disease; migraine; senile dementia; inflammatory disease; rheumatoid arthritis; autoimmune disorder; respiratory ailment;
                                                                                                                                                                                                                                                                                                                                                                  Slightom J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New G protein-coupled receptor (nGPCR-x) and its encoding polynucleotide useful for diagnosing and treating e.g. schizophrenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                     i LA, Hiebsch RR, Lind P, Sligh
Bannigan CM, Ruff V, Sejlitz T,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       261pp; English.
                                                                                                                                                                                                                                                                                                                                                                         Parodi LA,
                                                                                                                                                                                                                                                                                                     UPJOHN CO
                                  17-MAR-2000; 2000US 0190310.
21-MAR-2000; 2000US 0190800.
20-APR-2000; 2000US 0198568.
08-MAY-2000; 2000US 0201190.
25-MAY-2000; 2000US 02011190.
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                                                                                                                                                                                                                                                                                                                                                                                                        PS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           yative
                                                                                                                                                                                                                                                                                                                                                                             Wood LS,
A, Kaytes
20000S
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                                                                                                                                                                                                                                                                                                     (PHAA ) PHARMACIA 6
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Best Local Similarity
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Schellin KA,
   09-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-AUG-2001
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(first entry)

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G protein-coupled receptor; nGPCR; seven transmembrane receptor; signal transduction; schizophrenia; thyroid disorder; renal failure; rheumatoid arthritis; CNS disorder; infection; metabolic disease; cardiovascular disease; proliferative disorder; hormonal disorder; neurological disorder; neuronal disorder; Alzheimer's disease; cancer; attention deficit thyperactivity disorder/attention deficit disorder; Parkinson's disease; migraine; senile dementia; inflammatory disease; rheumatoid arthritis; autoimmune disorder; respiratory allment;
                                        AAH51051 standard; DNA; 20 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (PHAA ) PHARMACIA & UPJOHN CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-NOV-2000; 2000WO-US31581
                                                                                                                                                        Oligonucleotide SEQ ID 131
                                                                                                                                                                                                                                                                                                                                                neuroprotective; ss
                                                                                                                                                                                                                                                                                                                                                                                                                            WO200136473-A2.
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21-MAR-2000;
20-APR-2000;
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02-MAR-2000;
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08-MAY-2000;
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19-NOV-1999;
28-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-FEB-2000;
                                                                                                                  28-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                            AAH51051;
                      AAH51051/c
                                                                            The present invention relates to novel G protein-coupled receptors

(nGPCRX: where x is 1, 3, 4, 5, 9, 11, 12, 14-18, 20, 21, 22, 24, 27,
28, 31-38, 40, 41, 53-60) and their coding sequences (see
28, 31-38, 40, 41, 53-60) and their coding sequences (see
present sequence is a PCR primer, which was used in an example from the
present invention. GPCRs are also known as seven transmembrane receptors
and function in signal transduction. The nGPCRx coding sequences are
useful for screening a human to diagnose a disorder affecting the brain
or a genetic predisposition, specifically schizophrenia. nGPCRx are
useful for identifying compounds useful for treating schizophrenia.
Detection of nGPCRx in a sample is useful as a diagnostic tool for
diseases or disorders e.g. thyroid disorders, renal failure, rheumatoid
arthritis, CNS disorders, infections such as HIV1, metabolic and
cardiovascular diseases, proliferative disorders and hormonal disorders.
Modulators of nGPCRx activity have the utility for treating neurological
disorders und schizophrenia, ADHD/ADD (attention deficit-
disorders such as Alzheimer's disease, Parkinson's disease, migraine and
senile dementia. Additional disorders include inflammatory conditions
(e.g. Crohn's disease), rheumatoid arthritis, autoimmune disorders,
cancers, respiratory aliments such as asthma, and inflammatory diseases
e.g. inflammatory bowel disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Parodi LA, Hiebsch RR, Lind P, Slightom J;
PS, Bannigan CM, Ruff V, Sejlitz T, Huff RM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New G protein-coupled receptor (nGPCR-x) and its encoding polynucleotide useful for diagnosing and treating e.g. schizophrenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 20 BP; 5 A; 7 C; 4 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 4; Page 117; 261pp; English.
neuroprotective; PCR primer; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (PHAA ) PHARMACIA & UPJOHN CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-MAY-2000; 2000US-0207094.
                                                                                                                                                                                                                                                                                                                            2000US-0186530
                                                                                                                                                                                                                                                                                                                                                                                                                        20-APR-2000; 2000US-0198568.
02-MAY-2000; 2000US-0201190.
                                                                                                                                                                                                                                                                    2000US-0184129
2000US-0185421
                                                                                                                                                                                                                                                                                                                                                                                      2000US-0190310
                                                                                                                                                                                                              99US-0166071
99US-0166678
                                                                                                                                                                                                                                                    99US-0173396
                                                                                                                                                                                                                                                                                                                                                                                                      21-MAR-2000; 2000US-0190800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-0203111
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                                                                                                                                                                                                                                                                                                          2000US-0185554
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wood LS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-389826/41.
                                                                          WO200136473-A2.
                                                                                                                                                                                                                            19-NOV-1999;
28-DEC-1999;
22-FEB-2000;
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                                        Homo sapiens.
                                                                                                                                                    16-NOV-2000;
                                                                                                                                                                                                                                                                                    28-FEB-2000;
28-FEB-2000;
                                                                                                                                                                                                                                                                                                                            02-MAR-2000;
                                                                                                                                                                                                                                                                                                                                            03-MAR-2000;
09-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                    17-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-MAY-2000;
                                                                                                              25-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vogeli G,
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2000US-0186530

2000US-0184129

2000US-0185421 2000US-0185554

2000US-0190310 2000US-0190800 2000US-0198568 2000US-0207094

2000US-0186811 2000US-0188114

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CORPCRX; where x is 1, 3, 4, 5, 9, 11, 12, 14-18, 20, 21, 22, 24, 27, 28, 31-38, 40, 41, 53-60) and their coding sequences (see AAH551015 and AAH51105 and AAH680975 and AAG80977. The present sequence is an oligonucleotide, which was used in the present invention. GPCRs are also known as seven transmembrane receptors and function in signal transduction. The nGPCRx coding sequences are useful consention in signal transduction. The nGPCRx coding sequences are useful consention in signal transduction. The nGPCRx coding sequences are useful consenting a human to diagnose a disorder affecting the brain or a genetic predisposition, specifically schizophrenia. Detection of conference in conference in sample is useful for treating schizophrenia. Detection of disorders infections such as HIV-1, metabolic and cardiovascular cliseases, proliferative disorders and hormonal disorders. Modulators of nGPCRx activity have the utility for treating neurological disorders of nGPCRx activity have the utility for treating neurological disorders.
Parodi LA, Hiebsch RR, Lind P, Slightom J;
PS, Bannigan CM, Ruff V, Sejlitz T, Huff RM;
                                                                                                                                                                                                                                                               New G protein-coupled receptor (nGPCR-x) and its encoding polynucleotide useful for diagnosing and treating e.g. schizophrenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               present invention relates to novel G protein-coupled receptors
                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 245; 261pp; English.
                                                           Kaytes
     Wood LS,
                                                                                                                                                             WPI; 2001-389826/41
                                                      Schellin KA,
Vogeli G,
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Gaps

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0; Indels

1.9%; Score 20; DB 22; Length 20;

9.4;

100.08;

0; Mismatches Pred. No.

327 GGCTGCGGACAGGTATTTCA 346

õ a

20; Conservative

Local Similarity

Query Match Matches 20 GGCTGCGGACAGGTATTTCA 1

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Example 11; Page 143; 261pp; English.
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\overset{\circ}{\mathsf{A}}\overset{\circ}{\mathsf{X}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\overset{\circ}{\mathsf{C}}\over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                             Alzhelmer's disease, Parkinson's disease, migraine and senile dementia. Additional disorders include inflammatory conditions (e.g. Crohn's disease), rheumatoid arthritis, autoimmune disorders, cancers, respiratory aliments such as asthma, and inflammatory diseases e.g. inflammatory bowel disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     signal transduction; schizophrenia; thyroid disorder; renal failure; rheumatoid arthritis; CNS disorder; infection; metabolic disease; cardiovascular disease; proliferative disorder; hormonal disorder; hormonal disorder; hormonal disorder; attention deficit-hyperactivity disorder; Alzheimer's disease; cancer; attention deficit-hyperactivity disorder/attention deficit disorder; parkinson's disease; migralne; senile dementia; inflammatory disease; rheumatoid arthritis; autoimmune disorder; respiratory ailment; neuroprotective; PCR primer; ss.
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disorder/attention deficit disorder), and neuronal disorders such as
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Bannigan CM, Ruff V, Sejlitz T, Huff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein-coupled receptor; nGPCR; seven transmembrane receptor;
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                                                                                                                                                                                                                                                                                                                                                                                                                      Score 20; DB 22; Length 20; Pred. No. 9.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                              Sequence 20 BP; 5 A; 8 C; 3 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human nGPCR11 PCR primer LW1661.
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 1.9%; Sco
Best Local Similarity 100.0%; Pi
Matches 20; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   od LS, Parodi LA,
Kaytes PS, Bannic
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99US-0166678.
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2000US-0186530.
2000US-0186811.
2000US-0188114.
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2000US-0198568.
2000US-0201190.
2000US-0203111.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200136473-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-FEB-2000;
02-MAR-2000;
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28-FEB-2000;
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8$88888$8
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                                                                                                                                                                                                                                                                                                                                         , respiratory ailments such as asthma, and inflammatory diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                        Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                      Score 20; DB 22;
Pred. No. 9.4;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                          1.9%,
100.0%; Pic
                                                                                                                                                                                                                                                                                                                                                        e.g. inflammatory bowel disease.
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9905-0166771
9905-016678.
9905-0173396
200005-0184129.
200005-018554.
200005-0186530.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oligonucleotide SEQ ID 132.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-AUG-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
Best Local Similarity 100.
Matches 20; Conservative
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03-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-NOV-1999;
19-NOV-1999;
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Homo sapiens.
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                                                                                                                                                                                                                                                                                        The present invention relates to novel G protein-coupled receptors

(nGPCRx; where x is 1, 3, 4, 5, 9, 11, 12, 14-18, 20, 21, 22, 24, 27, 28, 31-38, 40, 41, 53-60) and their coding sequences (see

28, 31-38, 40, 41, 53-60) and their coding sequences (see

AAR15096-AAH51015 and AAH51015 and AAG80929-AAG80975 and AAG80977). The

present sequence is an oligonuclectide, which was used in the present

invention. GPCRs are also known as seven transmembrane receptors and

function in signal transduction. The nGPCRx coding sequences are useful

for screening a human to diagnose a disorder affecting the brain or a

genetic predisposition, specifically schizophrenia. nGPCRx are useful

for identifying compounds useful for treating schizophrenia. Detection of

CRS disorders e.g. thyroid disorders, renal failure, rheumatoid arthritis,

CRS disorders, infections such as HIV-1, metabolic and cardiovascular

diseases, proliferative disorders and hormonal disorders. Modulators of

crock at including schizophrenia, ABHPARD (attention deficit disorders), and neuronal disorders such as

Alzheimer's disease, Parkinson's disease, migraine and senile dementia.

CR Additional disorders include inflammatory conditions (e.g. Crohn's

Alexana) Alexana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          signal transduction; schizophrenia; thyroid disorder; renal failure; rheumatoid arthritis; CNS disorder; infection; metabolic disease; cardiovascular disease; proliferative disorder; hormonal disorder; neurological disorder; rheumatoid arthritis; autolimmune disorder; respiratory disease; neuroprotective; PCR primer; ss.
                                                                                                                                               Vogeli G, Wood LS, Parodi LA, Hiebsch RR, Lind P, Slightom J;
Schellin KA, Kaytes PS, Bannigan CM, Ruff V, Sejlitz T, Huff RM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                       New G protein-coupled receptor (nGPCR-x) and its encoding polynucleotide useful for diagnosing and treating e.g. schizophrenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  disease), rheumatoid arthritis, autoimmune disorders, cancers, respiratory ailments such as asthma, and inflammatory diseases e.g. inflammatory bowel disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             G protein-coupled receptor; nGPCR; seven transmembrane receptor;
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 48 BP; 14 A; 15 C; 10 G; 9 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Pred. no.
                                                                                                                                                                                                                                                                 Disclosure; Page 246; 261pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human nGPCR11 PCR primer LW1659.
                                                                                                                  (PHAA ) PHARMACIA & UPJOHN CO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   962 GGAGTTGCATCAGTGTGGCA 981
                                        20-APR-2000; 2000US-0198568.
02-MAY-2000; 2000US-020190.
08-MAY-2000; 2000US-0203111.
25-MAY-2000; 2000US-0207094.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48 GGAGTTGCATCAGTGTGGCA 29
                             2000US-0190800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20; Conservative
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                                                                                                                                                                                           WPI; 2001-389826/41
          17-MAR-2000;
21-MAR-2000;
                                                                                                                                              Vogeli G,
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The present invention relates to novel G protein-coupled receptors

(nGPGRx; where x is 1, 3, 4, 5, 9, 11, 12, 14-18, 20, 21, 22, 24, 27,

(28, 31-38, 40, 41, 53-60) and their coding sequences (see
ANH50969-ANH51015 and ANH51105 and AAG80975 and AAG80977). The
present sequence is a PCR primer, which was used in an example from the
present invention. GPCRs are also known as seven transmembrane receptors
and function in signal transduction. The nGPCRs coding sequences are
useful for screening a human to diagnose a disorder affecting the brain
or a genetic predisposition, specifically schizophrenia. nGPCRs are
useful for identifying compounds useful for treating schizophrenia.

C a genetic predisposition, specifically schizophrenia chiscopters
or a genetic predisposition, specifically as a diagnostic tool for
diseases or disorders e.g. thyroid disorders, renal failure, rheumatoid
cardiovascular diseases, proliferative disorders and hormonal disorders
c disorders, infections such as HIV-1, metabolic and
cardiovascular diseases, proliferative disorders and hormonal disorders
disorders, including schizophrenia, ANHD/ADD (attention deficition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hyperactivity disorder/attention deficit disorder), and neuronal disorders such as Alzheimer's disease, Parkinson's disease, migraine and senile dementia. Additional disorders include inflammatory conditions (e.g. Crohi's disease), rheumatoid arthritis, autoimmune disorders, cancers, respiratory ailments such as asthma, and inflammatory diseases e.g. inflammatory bowel disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vogeli G, Wood LS, Parodi LA, Hiebsch RR, Lind P, Slightom J;
Schellin KA, Kaytes PS, Bannigan CM, Ruff V, Sejlitz T, Huff RW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New G protein-coupled receptor (nGPCR-x) and its encoding polynucleotide useful for diagnosing and treating e.g. schizophrenia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 48 BP; 14 A; 15 C; 10 G; 9 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 11; Page 143; 261pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (PHAA ) PHARMACIA & UPJOHN CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        962 GGAGTTGCATCAGTGTGCCA 981
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                                                                                                                                                                                                                                                                                                                                                                                                  2000US-0185421.
2000US-0185554.
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2000US-0186811
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2000US-0190310.
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Best Local Similarity 100.
Matches 20; Conservative
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WO200136473-A2.
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28-FEB-2000;
02-MAR-2000;
03-MAR-2000;
09-MAR-2000;
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20-APR-2000;
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2000US-0232081.
2000US-023399.
2000US-0232399.
2000US-0232399.
2000US-0232400.
2000US-0232400.
2000US-0233064.
2000US-0234063.
2000US-0234099.
2000US-0234997.
2000US-0234997.
2000US-0234997.
2000US-0234997.
2000US-0234997.
2000US-0234997.
2000US-0236368.
2000US-0236368.
2000US-0236369.
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20000S-0239937
20000S-0241221
20000S-0241785
20000S-0241786
20000S-0241786
20000S-0241808
20000S-0241809
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20000S-0241809
20000S-024647
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20000S-0246528
20000S-0246538
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2000US-0249209.
2000US-0249210.
2000US-0249211.
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2000US-0249297.
2000US-0249299.
       2000US-0232080
    08 - SEP - 2000; 20 - SEP - 2000; 20 - SEP - 2000; 21 - SEP - 2000; 21 - SEP - 2000; 21 - SEP - 2000; 22 - SEP - 2000; 22 - SEP - 2000; 23 - SEP - 2000; 24 - SEP - 2000; 25 - SEP - 2000; 26 - SEP - 2000; 26 - SEP - 2000; 27 - 2000; 27 - SEP - 2000; 27 - 2000; 27 - SEP - 2000; 2
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17 - NOV - 2000;
17 - NOV - 2000;
17 - NOV - 2000;
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17-NOV-2000;
       Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparaaitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein; musculoskeletal system; ds.
                                                                                                Human musculoskeletal system related polynucleotide SEQ ID NO 3513
AAL37148/c
ID AAL37148 standard; DNA; 4715 BP.
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2000US-022513
2000US-0225213
2000US-022526
2000US-022526
2000US-022526
2000US-0225276
2000US-0225757
2000US-0225757
2000US-0225757
2000US-022568
2000US-022688
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2000US-0228934
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2000US-0180628
2000US-018464.
2000US-0189874.
2000US-0199076.
2000US-0199076.
2000US-0199067.
2000US-020515.
2000US-0215135.
2000US-0215135.
2000US-0215135.
2000US-0217496.
2000US-0217496.
2000US-0217496.
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2000US-0231242.
2000US-0231244.
2000US-0231244.
2000US-0231413.
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                                                                      (first entry)
                                                                                                                                                                                                                                              WO200155367-A1.
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04-FEB-2000;
02-FEB-2000;
02-MAR-2000;
11-MAR-2000;
11-MAR-2000;
19-MAY-2000;
07-JUN-2000;
07-JUN-2000;
30-JUN-2000;
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14 - AUG - 2000)
18 - AUG - 2000)
18 - AUG - 2000)
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22-AUG-2000;
23-AUG-2000;
30-AUG-2000;
01-SEP-2000;
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-SEP-2000;
-SEP-2000;
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                                                                                                                                                                                                                       saptens
                                                                      08-JAN-2002
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                                           AAL37148
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40200171042-A2.
            WO200171042-A2.
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                                   27-SEP-2001
                                                                                                                                                Penter JC,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                             The invention relates to novel genes (AAL34669-AAL37666) and proteins (ABB03087-ABB04109) associated with the musculoskeletal system useful for preventing, treating or ameliocating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (anti-agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune cancers e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disonders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral snoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                          Isolated polypeptide for treating, preventing and/ or prognosing disorders related to the musculoskeletal system including musculoskeletal cancers and also for testing and detection e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila; developmental biology; cell signalling; insecticide;
pharmaceutical; gene; ds.
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                                                                                                                                                                                                                                                                                                                        Example 2; SEQ ID NO 3513; 781pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.9%; Score 20; DB 22; Length 4715;
100.0%; Pred. No. 9;
tive 0; Mismatches 0; Indels (
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                                                                                                                                                                                                             Barash SC, Ruben SM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCTTATGATCTGCCTGCCTT 208
                                 2000US-0251030.
2000US-0251988.
2000US-0256719.
2000US-0251479.
                                                                                              2000US-0251868.
2000US-0251869.
2000US-0251989.
                                                                                                                                 08-DEC-2000; 2000US-0251990.
11-DEC-2000; 2000US-0254097.
05-JAN-2001; 2001US-0259678.
                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC
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ID ABL17061 standard; DNA; 912
                       2000US-0250391
                                                                                   2000US-0251856
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                               05-DEC-2000; 2
05-DEC-2000; 2
06-DEC-2000; 2
08-DEC-2000; 2
08-DEC-2000; 2
08-DEC-2000; 2
08-DEC-2000; 2
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capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ABB57737-ABB72072).
The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.w1po.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                 New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              developmental biology; cell signalling; insecticide;
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100.0%; Pred. No. 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      claim 1; SEQ ID NO 2656; 21pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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11-JUL-2000; 2000US-0614150.
                                                  23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
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23-MAR-2001; 2001WO-US09231
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hes 19; Conservative
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                                                                                                                                                                                                                                                                     PI; 2001-656860/75
                                                                                                                                                    (PEKE ) PE CORP NY.
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Gaps

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0; Indels

Score 19; DB 23; Pred. No. 29; 0; Mismatches 0

Length 2977;

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The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).
                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster genomic polynucleotide SEQ ID NO 9727.
                                                                                                   Sequence 2977 BP; 845 A; 616 C; 680 G; 836 T; 0 other;
                                                                                                                                                                                                                                                                                418/c
ABL19418 standard; DNA; 3482 BP.
                                                                                                                               Query Match 1.8%; Soc
Best Local Similarity 100.0%; P:
Matches 19; Conservative 0;
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                                                                                                                                                                                                         1041 ATGAACAGCATGCTGGATC 1023
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11-JUL-2000; 2000US-0614150.
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Best Local Similarity 100.
Matches 19; Conservative
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                                                                                                                              The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryottes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLiol3640-ABLiol575) and the encoded proteins
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                                                                                                                                                                                                                                               The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.w1po.lnt/pub/published_pct_sequences.
                                             New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
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                                                                                                   Claim 1; SEQ ID NO 809; 21pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                           Sequence 2947 BP; 772 A; 921 C; 719 G; 535 T; 0 other;
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Pred. No. 29;
0; Mismatches
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100.0%; Pre
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ID ABL17060 standard; DNA; 2977 BP
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11-JUL-2000; 2000US-0614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                        sequences (ABL01840-1
(ABB57737-ABB72072).
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WPI; 2001-656860/75.
P-PSDB; ABB58006.
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Matches
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New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                           The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA
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                                                                                                                                                       Claim 1; SEQ ID NO 9727; 21pp + Sequence Listing; English.
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100.0%; Pred. No. 28;
ive 0; Mismatches
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Myers EW;

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20000S-0241787.
2000US-0241808.
2000US-0241808.
2000US-0241826.
2000US-0246475.
2000US-0246477.
2000US-0246477.
2000US-0246477.
2000US-0246523.
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2000US-0231414.
2000US-0232080.
2000US-0232080.
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2000US-0232397.
2000US-0232398.
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2000US-0232400.
2000US-0232401.
2000US-0233063.
2000US-0233064.
2000US-0233064.
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2000US-0234997.
2000US-0234998.
2000US-0235484.
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2000US-0235836.
2000US-0236327.
2000US-0236367.
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2000US-0237037.
2000US-0237038.
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2000US-0239935.
2000US-0239937.
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2000US-0241785.
2000US-0241786.
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2000US-0249213.
2000US-0249214.
2000US-0249215.
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05 SEP - 2000;

06 SEP - 2000;

08 SEP - 2000;

14 SEP - 2000;

15 SEP - 2000;

16 SEP - 2000;

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19 SEP - 2000;

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11 SEP - 2000;

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13 SEP - 2000;

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24 SEP - 2000;

25 SEP - 2000;

27 SEP - 2000;

28 SEP - 2000;

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29 SEP - 2000;
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    Neuroprotective; cytostatic; dermatological; immunosuppressive; tumour; antilnflammatory; anti-HIV; antibacterial; antilnflammatory; cancer; immune system disorder; rheumatoid arthritis; inflammatory condition; organ transplant rejection; infection; hepatitis; or blood disorder; sickle cell anaemia; hyperproliferative disorder; Gaucher's disease; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; chromosomal abnormality; Down syndrome; ischaemia; renal disorder; reproductive system; gastrointestinal; ilver disorder; Addison's disease; acquired immune deficiency syndrome.
                                                                                                                                                                                        DNA encoding novel signal transduction pathway protein, Seq ID 1482.
                                                                                            AAS27822 standard; DNA; 10098 BP
 3212 ATGAACAGCATGCTGGATC 3194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20000S-0220963.
20000S-0224519.
20000S-0224519.
20000S-0225213.
20000S-0225266.
20000S-0225266.
20000S-0225267.
20000S-0225267.
20000S-022547.
20000S-0225759.
20000S-0225759.
20000S-0225759.
20000S-0225759.
20000S-0225759.
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2000US-0229345
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                                                                                                                                                                                                                                                                                                                                                                                                                             WO200154733-A1
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14-AUG-2000; 2
14-AUG-2000; 2
18-AUG-2000; 2
22-AUG-2000; 2
22-AUG-2000; 2
23-AUG-2000; 2
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14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
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                                                                                                                           AAS27822;
                                                                             AAS27822
                                                              RESULT
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Low density lipoprotein binding protein 1; LBP-1; LDL; human; atherosclerosis; antiarteriosclerotic; gene therapy; diagnosis;
                                                                                   Human low density lipoprotein binding protein 1 (LBP-1) gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BOST-) BOSTON HEART FOUND INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-FEB-2001; 2001WO-US06356.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-MAR-2000; 2000US-0517849
14-JUL-2000; 2000US-0616289
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P-PSDB; AAB82802.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200164874-A2.
                                                                                                                                                                                            Homo sapiens.
                                                 12-NOV-2001
                                                                                                                                                         vaccine; ds.
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                AAH26493;
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                                                                                                                                                                                                                              Key
The invention relates to novel isolated polypeptides (I); and display to (I) are useful for displaying languages (II). (I), (II) and the antibody to (I) are useful for displaying inmunosing, preventing and treating diseases including immune system disorders (e.g. congenital and acquired immunodeficiencies, autoimmune transplant rejections and graft versus host disease, infectious diseases (e.g. hepatitis C), bleeding disorders, heamoglobin abnormalities and there blood related disorders (etcher blood related disorders (etcher blood related disorders (etcher blood related disorders (etcher blood related) in disorders, hyperproliferative disorders (e.g. daucher's disease, Parkinson's disease), chromosomal abnormalities (bown syndrome), ischaemic injury (e.g. stroke), renal disorders (e.g. stroke), respiratory disorders, dermacological disorders (e.g. arrhythmia), respiratory disorders, dermacological disorders (e.g. arrhythmia), respiratory disorders, dermacological disorders (e.g. arrhythmia), respiratory disorders, dermacological disorders (adsorder (inflammatory disorders), liver disorders (cirrhosis), as stimulators of B-cell responsiveness to pathogens, activators of treals, to induce higher affinity antibodies, and as a means to induce tumour proliferation in pathologies e.g. acquired immune deficiency syndrome (AIDS). AAS26976-AAS22800 represent novel signal transduction cpathway protein coding sequences and PCR primers of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel polypeptides useful for diagnosing, treating, preventing and/or prognosing disorders related to the proteins, including cancers, immune disorders and neuronal disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 22; Length 10098; . 28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.8%; Score 19; DB 00.0%; Pred. No. 28; ve 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID No 1482; 880pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rosen CA, Barash SC, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                       (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                      2001US-025967B.
                                                                                                                                                       2000US-0249300
2000US-0250160
                                                                                                                                        2000US-0249299
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                                                                                                                      2000US-0249297
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01-DEC-2000;
01-DEC-2000;
05-DEC-2000;
05-DEC-2000;
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06-DEC-2000;
08-DEC-2000;
08-DEC-2000;
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08-DEC-2000;
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17-NOV-2000;
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8075..10902 /\*tag= g 10903..10965

'anticodon=

7898..8074 \*tag= \*tag=

/cons\_splice= "(5'site:No, 3'site:No)" 5382.:5453 /\*tag= d 5454..7897

/\*tag= a /note= "includes introns" 2875..3018

b .19..5381 /\*tag= r 'cone

Location/Qualifiers 2875..10965

(first entry)

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The present sequence is that of genomic DNA encoding novel human low density lipoprotein binding protein 1 (LBP-1, see AAB82802).

The DNA was isolated from a human genomic library by screening with LBP-1 cDNA (see AAH26492). The open reading frame spans 4 exons. Human LBP-1 nucleic acids are among claimed polynucleotides of the invention that encode novel polypeptides, termed LBPs, capable of binding to native and methylated LDL. Also claimed are isolated LBP polypeptides, and biologically active fragments and analogues of them, as well as expression vectors, cells and methods of producing the LBPs. Methods of determining if an animal is at risk for atherosclerosis, methods for evaluating an agent for use in abnormality in structure or metabolism of LBP are claimed.

Characterized compositions comprising an LBP polypeptide or nucleic acid, and vaccine compositions, are also claimed.
New isolated low density lipoprotein binding polypeptide for treating, diagnosing and/or identifying therapeutic agents for atherosclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 12619 BP; 3743 A; 2541 C; 2359 G; 3976 T; 0 other;
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Gaps

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0; Indels

100.08;

AAH26493 standard; DNA; 12619 BP.

RESULT 33 AAH26493 ID AAH264

2433 CCTTATGATCTGCCTGCCT 2451

189 CCTTATGATCTGCCTGCCT 207

à

Law SW, Arjona AA;

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C195_1 protein; human PBWC cDNA library; cytokine activity; ss; peripheral blood mononuclear cell; nutritional activity; homology; cell proliferation/differentiation activity; EST; expressd sequence tag.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Poly:nucleotide(s) and proteins obtained from human PBMC, dendritic cell, adult brain, foetal brain and adult testes cDNA libraries - used in research, detection and therapy of, e.g. cytokine and cell proliferation or differentiation
                                                         Nucleotide sequence of the 5' portion of the C195_1 protein.
                                                                                                                                                                                      /*tag= a
/product= "C195_1 protein"
/note= "no stop codon found at the 3' end"
                                                                                                                                                                                                                                                                                                                                                                           Evans C, Jacobs K, LaVallie ER, Racie LA, Spaulding V, Treacy M;
                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 47; 78pp; English.
                                                                                                                                                                                                                                                                                               97WO-US10501
                                (first entry)
                                                                                                                                                                                                                                                                                                                                                  (GEMY ) GENETICS INST INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
Best Local Similarity
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P-PSDB; AAW42074.
                                                                                                                                      sapiens
                                                                                                                                                                                                                                            WO9748801-A2
                                                                                                                                                                                                                                                                                             16-JUN-1997;
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                                07-JUL-1998
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Merberg D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-JUN-1998
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      AAV09268;
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ID AAV042

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XX 22-JUN

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL016175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wlpo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions \cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                Gaps
                                                                                                                                                                                                                                                      Drosophila; developmental biology; cell signalling; insecticide;
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                                                                                                                                                                                                                            Drosophila melanogaster expressed polynucleotide SEQ ID NO 806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.8%; Score 19; DB 23; Length 19175; Similarity 100.0%; Pred. No. 28; Conservative 0; Mismatches 0; Indels 0
DB 22; Length 12619;
28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 806; 21pp + Sequence Listing; English.
                               Indels
                               ;
0
                               Mismatches
    1.8%; Score 19;
100.0%; Pred. No.
:ive 0; Mismatch
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                                                                                                                                                ABL02108 standard; cDNA; 19175
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                                                                    Db 1940 CCTTTCCCAAATTCTACAA 1958
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                                                       CCTTTCCCAAATTCTACAA 869
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11-JUL-2000; 2000US-0614150.
                                                                                                                                                                                                                                                                                                                                                                        23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                  (first entry)
                               Conservative
                                                                                                                                                                                                                                                                  pharmaceutical; gene; ss.
                                                                                                                                                                                                                                                                                           Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-656860/75.
P-PSDB; ABB58005.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          (PEKE ) PE CORP NY.
                 Similarity
                                                                                                                                                                                                                                                                                                                     WO200171042-A2.
                                                                                                                                                                                                                                                                                                                                              27-SEP-2001.
                                                                                                                                                                                                  26-MAR-2002
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     Query Match
                                                                                                                                                                        ABL02108;
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Best Local 3
                    Local
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AAV09268/c
ID AAV092
XX
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Matches
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MCCOY JM;

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This nucleotide sequence encodes the 5' portion of the C195_1 protein which was isolated from a human PBMC CDNA library. The products of the polynucleotides of the invention can be used in research, detection and therapy, as they may have nutritional activity, cytokine and cell prollferation/differentiation activity. A search against the Genbank database demonstrated that this sequence has at least some homology with two ESTs identified as "ygl1906.rl Homo sapiens CDNA clone 19937 5'" and "yml5f12.rl Homo sapiens CDNA clone 48025 5'".
                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Secreted protein; C195_1; peripheral blood mononuclear cell; PBMC; protein factor; human; ds.
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                                                                                                                                                                                                                                                                                                                     Score 18; DB 19; Length 433;
Pred. No. 92;
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                                                                                                                                                                                                                                                                  Sequence 433 BP; 125 A; 85 C; 98 G; 125 T; 0 other;
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Mismatches
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100.0%; Pre
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                                                                                                                                                                                                                                                                                                                                                                                                                                        531 TGACATCATGTTCCAGCT 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      341 TGACATCATGTTCCAGCT 324
                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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Homo saptens

16-JUN-1997;

24-DEC-1997

17-JUN-1996; 27-SEP-1996; 25-OCT-1996;

WO9748800-A1

mat\_peptide

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The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, memaropolesis regulating activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                         Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopolesis; tissue growth factor; immunomodulatory; cancer; leukaemla; nervous system disorders; arthritis; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Expressed sequence tag; secreted protein; haematopolesis regulator; tissue growth; activin; inhibin; tumour invasion suppressor; EST; human; chemotaxis; chemokinesis; haemostasis; gene therapy; thrombolysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemla, inflammation and immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 12534; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 444 BP; 88 A; 110 C; 108 G; 138 T; 0 other;
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Pred. No. 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Pred. ....
                                                              Human polynucleotide SEQ ID NO 12534.
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ID AAV86048 standard; cDNA; 451 BP.
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18-MAY-2000; 2000US-0577409.
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                   (first entry)
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-514838/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tang YT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; AA012543.
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                                                                                                                                                                                                                                                                          WO200164835-A2
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                                                                                                                                                                                                                               Homo sapiens
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                   06-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This cDNA clone, designated C195_1, codes for a novel secreted protein (see AAW41600) of human peripheral blood mononuclear cells (PBMC). It was isolated from a PBMC cDNA library using methods which are selective for cDNAs encoding secreted proteins. The 433 coling the polyA tail, is provided in AAV404275. C195_1, including the polyA tail, is provided in AAV404275. C195_1 is deposited as ATCC 98079, a composite clone. An additional isolate of C195_1, designated C195_4 (see AAV04274), is deposited as ATCC 98192. Both sequences can be recovered using a probe (see AAV04276). The isolated nucleic acid may be used to express recombinant secreted proteins; as a tissue/molecular weight marker; for chromosome identification; to identify possible genetic disorders; to isolate or anti-DNA antibodies; in interaction trap assays to identify sequences that encode interacting proteins etc. The secreted proteins can be used to screen compounds for biological activity; creceptors and ligands and as nutritional sources. They may also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       have biological activities, e.g. cytokine, cell proliferation or differentiation activity, immunosuppressant, immunostimulant, requiation of heamatopoiesis, modulation of fertility, chemotactic, chemokinetic, haemostatic, thrombolytic, antimicrobials, analgesic, antipsoriatic, etc. No evidence is given to support any of these
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acid encoding secreted protein from human peripheral blood mononuclear cells - useful, e.g. as immunomodulators, antitumour agents, promoters of tissue growth, haemostatic and thrombolytic agents etc.
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Spaulding V, Treacy M;
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                                                                Location/Qualifiers
13..433
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100.0%; Prev
0; F
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                                                                                                                                                                                                                                                                                                                       96US-0664596
96US-0721926
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                                                                                                                /*tag= a
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es 18; Conservative
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Gaps

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AAI92474 standard; cDNA; 444 BP.

RESULT 37 AAI92474

Query Match Matches

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AAI92474;

Length 444; 0; Indels

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The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polyneptides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, itssue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                     Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immune
                                                                                                                                                                                                                               Claim 1; SEQ ID NO 2799; 1399pp + Sequence Listing; English.
                                                                                          Drmanac RT
               28-FEB-2000; 2000US-0515126.
18-MAY-2000; 2000US-0577409.
                                                                                                                        WPI; 2001-514838/56.
                                                             (HYSE-) HYSEQ INC.
                                                                                          Liu C,
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                                                                                                                                                                                                   disorders
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                                                                                                                                                                                                                                                                                                                                                                              This sequence represents an expressed sequence tag (EST), and is a polynucleotide of the invention. The polynucleotides of the invention are all secreted EST sequences isolated from a variety of human tissue sources. The EST sequences and proteins encoded by them are predicted to have useful biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting dat is given. Suggested activities include nutritional activity, tissue given. Suggested activities haematopoiesis regulating activity, tissue growth activity, activity, activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, cadherin/tumour invasion suppressor activity, tumour inhibition activity. The EST sequences are also stated to be useful for gene
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                                                                                                                                                                                                                                                                                       New polynucleotides encoding human secreted proteins - derived from e.g. human blood, kidney, foetal lung, placenta, testes, brain, ovary, pituitary, retina and colon cDNA libraries
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                                                                                                                                                                                                               J, Jacobs K, Lavallie ER, McCoy JM, Merberg D;
Spaulding V, Treacy M;
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100.0%; Pred. No. 92;
ive 0; Mismatches 0; Indels
receptor; ligand; anti-inflammatory; tumour inhibitor; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 451 BP; 128 A; 91 C; 102 G; 130 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 101; 633pp; English.
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                                                                                                                       98WO-US06954.
                                                                                                                                                   97US-0835913.
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                               Homo sapiens
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                                                                                                                     10-APR-1998;
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                                                                                        15-0CT-1998
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                        DB 22; Length 464;
92;
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                                                                                                                                                                                                                                             100.0%; Pred. No. 92; tive 0; Mismatches
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Best Local Similarity 100.0
Matches 18; Conservative
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000005-0179065 000005-0180628 000005-0186350 00005-01989350 00005-0198076 00005-0198076 00005-0214886 00005-0216647 00005-0216880 00005-0216880 00005-0216880	20000S-0224518. 20000S-0224518. 20000S-0224513. 20000S-0225214. 20000S-0225267. 20000S-0225267. 20000S-0225270. 20000S-0225270. 20000S-0225270. 20000S-0225270. 20000S-0225270. 20000S-0225279. 20000S-0225279. 20000S-0225279. 20000S-0225279. 20000S-0225279. 20000S-0225279. 20000S-0229343. 20000S-0229343. 20000S-0229343. 20000S-0229343. 20000S-0229343.	0000US-0231244 0000US-0231241 0000US-0232080 000US-0232080 000US-0232399 000US-0232399 000US-0232399 000US-0232400 000US-0232400 000US-0232400 000US-0232400 000US-0232400 000US-023365 000US-023365 000US-02336370 000US-0235834 000US-0235834 000US-0235834 000US-0235834 000US-0235834
1-JAN-2000 2-MAR-2000 2-MAR-2000 3-MAR-	14-AUG-2000 14-AUG-2000 14-AUG-2000 14-AUG-2000 14-AUG-2000 14-AUG-2000 14-AUG-2000 14-AUG-2000 14-AUG-2000 14-AUG-2000 14-AUG-2000 14-AUG-2000 14-AUG-2000 14-AUG-2000 18-AUG-2000 18-AUG-2000 18-AUG-2000 18-AUG-2000 18-AUG-2000 19-AUG	8 - S - S - S - S - S - S - S - S - S -
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02-0CT-2000)
03-0CT-2000)
03-0C 

Š (HUMA-) HUMAN GENOME SCI INC

Ruben Barash SC, Rosen CA,

WPI; 2001-451930/48.

New cardiovascular system related polynucleotides and polypeptides, useful for diagnosing, treating and/or preventing disorders of the cardiovascular system -

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14-JUL-2000;
26-JUL-2000;
26-JUL-2000;
14-AUG-2000;
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18-AUG-2000;
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14-AUG-2000;
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25-SEP-2000;
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   Sequences AAS35741-AAS36942 represent genomic DNA molecules, which encode the cardiovascular system antigen polypeptides of the invention.

Cardiovascular system antigens and their associated polynucleotides are useful in the diagnosis, treatment and prevention of various types of disorders in e.g. humans, mice, rabbits, goats, horses, cats, dogs, colikens or sheep. A pathological condition can be determined by detecting the presence or absence of a mutation in a cardiovascular of diseases such as rheumatoid arthritis, hyperproliferative disorders such as neoplasms of the breast or liver, cardiovascular disorders such as neoplasms of the breast or liver, cardiovascular disorders such as cardiac arrest, cerebrovascular disorders such as cardiac arrest, cerebrovascular disorders such as corneal infection, endocrine disorders such as Alzheimer's disease, infections caused by bacteria, viruses and fungi, ocular disorders such as corneal infection, endocrine disorders such as premature labour and infertility, can galomerulonephritis and respiratory disorders such as asthma and pleurisy. The polypeptides can also be used to aid wound healing, to cream adjing due to sunburn, to maintain organs before cransplantation, but was obtained in electronic format directly from WIPO effert administration in the form part of the printed consideration or the partition of the administration of the printed consideration or the printed
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                           Claim 1; SEQ ID No 2262; 674pp; English.
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disorders in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. A pathological condition can be determined by detecting the presence or absence of a mutation in a cardiovascular system antigen polyfucleotide. The treatable disorders include autoimmune diseases such as rheumatoid arthritis, hyperproliferative disorders such as neoplasms of the breast or liver, cardiovascular disorders such as cardiovascular disorders such as cardiocascular disorders such as cardiocascular disorders such as cerebral ischaemia, nervous system disorders such as Alzheimer's disease, infections caused by bacteria, viruses and fundi, ocular disorders such as corneal infection, endocrine disorders such as premature labour and infertility, gastrointestinal disorders such as Crohn's disease, renal disorders such as glomerulonephritis and respiratory disorders such as asthma and pleurisy. The polypeptides can also be used to aid wound healing, to prevent skin aging due to sunburn, to maintain organs before transplantation, to regenerate tissues and in chemotraxis.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the wipo.int/published_pot_sequences.
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17-NOV-2000;
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01-DEC-2000;
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05-DEC-2000;
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08-DEC-2000;
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Ruben SM (HUMA-) HUMAN GENOME SCI INC Barash SC, Rosen CA,

WPI; 2001-451930/48. P-PSDB; AAU22367.

New cardiovascular system related polynucleotides and polypeptides, useful for diagnosing, treating and/or preventing disorders of the cardiovascular system -

Claim 1; SEQ ID No 526; 674pp; English.

Sequences AAS35126-AAS35740 represent cDNA molecules, which encode the cardiovascular system antigen polypeptides of the invention. Cardiovascular system antigens and their associated polynucleotides are useful in the diagnosis, treatment and prevention of various types of disorders in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. A pathological condition can be determined by detecting the presence or absence of a mutation in a cardiovascular system antigen polynucleotide. The treatable disorders include autoimmune diseases such as rheumatoid arthritis, hyperproliferative disorders such as neoplasms of the breast or liver, cardiovascular disorders such as

an additional isolate of clone C195\_1 (see AAV04273), deposited

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          nervous system disorders such as Alzheimer's disease, infections caused by bacteria, viruses and fungi, ocular disorders such as corneal infection, endocrine disorders such as premature labour and infertility, gastrointestinal disorders such as Crohn's disease, renal disorders such as glomerulonephritis and respiratory disorders such as asthma and pleurisy. The polypeptides can also be used to aid wound healing, to prevent skin aging due to sunburn, to maintain organs before transplantation, to regenerate tissues and in chemotaxis.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This cDNA clone, designated C195_4, codes for a novel secreted protein (see AAW41601) of human peripheral blood mononuclear cells (PBMC). It was isolated from a PBMC cDNA library using methods which are selective for cDNAs encoding secreted proteins. The 733 bps sequence represents the internal part of the clone; the 3' portion of C195_4, including the polyA tail, is provided in AAV04278, and the 5' portion in AAV04277. C195_4 is deposited as ATCC 98192.
cardiac arrest, cerebrovascular disorders such as cerebral ischaemia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acid encoding secreted protein from human peripheral blood mononuclear cells - useful, e.g. as immunomodulators, antitumour agents, promoters of tissue growth, haemostatic and thrombolytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Secreted protein; C195_4; peripheral blood mononuclear cell; PBMC; protein factor; human; ds.
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                                                                                                                                                                                                                      DB 22; Length 489;
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                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                      at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                    Pred. No.
                                                                                                                                                                                                                        Score 18;
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13..733
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96US-0664596.
96US-0721926.
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                                                                                                                                                                                                                                                                                        894 ACCCAAGCAGCCAGGACA 911
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                                                                                                                                                                                                                                      Best Local Similarity 100. Matches 18; Conservative
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/*tag=
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P-PSDB; AAW41601.
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17-JUN-1996;
27-SEP-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; neuroblastoma; malignancy; cancer; tumour marker; N-myc; TrkA; ss.
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              ARAV04776. The isolated clone acid may be used to express recombinant secreted proteins; as a tissue_molecular weight marker; for chromosome identification; to identify possible genetic disorders; to isolate related DNA, as a source of PCR primers; to generate anti-DNA antibodies; in interaction trap assays to identify sequences that encode interacting proteins etc. The secreted proteins can be used to screen compounds for biological activity; to raise antibodies; as tissue markers; for isolation of related receptors and ligands and as nutritional sources. They may
                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                         related receptors and ligands and as nutritional sources. They may also have biological activities, e.g. cytokine, cell proliferation or differentiation activity, immunosuppressant, immunostimulant, regulation of haematopolesis, modulation of fertility, chemotactic, chemokinetic, haemostatic, thrombolytic, antimicrobials, analgesic, antimisorialic, etc. No evidence is given to support any of these
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100.0%; Pred. No. 92;
iive 0; Mismatches 0; Indels
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Best Local Similarity 100.
Matches 18; Conservative
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The present invention describes methods of obtaining immunogenic proteins from Neisseria genomic sequences. AAA81453 to AAA82414

Crepresent specifically claimed Neisseria meningitidis genomic DNA sequences; AAA81260 to AAA8130 and AAB2560 to AAB2563 represent Sequences; AAA81259 and AAA8130 to AAA8131 represent PCR primers used in the isolation of Neisseria meningitidis MenB polynucleotide ORF Sequences, which are all used in the exemplification of the present composition. The nucleic acid sequences, protein sequences, and antibodies against them, can be used in the manufacture of a composition. The nucleic acid sequences, protein sequences, and antibodies against them, can be used in the manufacture of a composition of the present composition on be used an endicament (or in the manufacture of a medicament) for treating, preventing or diagnosing infection due to Neisserial bacteria. For example, some of the identified proteins could composition of vactories against mail also facilitate production of sequences and/or against all pathogenic Neisseriae. Identification of sequences from the bacterium will also facilitate production of biological probes, and mitivalent vaccines have also been tried but none have successfully corrected antigonic variability. The provision of further, complete sequences may provide an opportunity to identify secreted or surface expendences may provide an opportunity to identify secreted or surface exposed proteins that may be presumed targets for the immune system and which are not antigenically variable or at least more conserved than
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Ratti G, Scarselli M, Scarlato V;
                                                                                                                                                                                                                                                                                                                                                                          Neisseria meningitidis; Neisseria gonorrheae; genome; immunogenic;
antigen; vaccine; diagnosis; infection; antibacterial; identification;
Meningococcus B; MenB; ds
                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated nucleotide sequences of Neisseria meningitidis which can be used in the diagnosis and treatment of N. meningitidis infection and other Neisserial infections, for example, N.gonorrhoea -
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    DB 22; Length 757; 92;
                                                                                                                                                                                                                                                                                                                                       N. meningitidis partial DNA sequence gnm_139 SEQ ID NO:139.
                                           0; Indels
  1.7%; Score 18; DB
100.0%; Pred. No. 92;
iive 0; Mismatches
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C, Mora M,
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ID AAA81592 standard; DNA; 767 BP.
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99US-0132068
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Query Match 1.7
Best Local Similarity 100.
Matches 18; Conservative
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Masignani V, Galeotti
Rappuoli R, Pizza M;
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                           Sequence 767 BP; 215 A; 144 C; 155 G; 253 T; 0 other;
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                                                                     100.0%; Pred. No. 92; tive 0; Mismatches
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Job time : 247 secs
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other more variable regions.
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Matches 18; Conserv
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AX148182 Sequence
AX299705 Sequence
AX338371 Sequence
AX398371 Sequence
AX305131 Sequence
AX305131 Sequence
AX205131 Homo sapi
AX277635 Sequence
AX277635 Sequence
AX277635 Sequence
AX148194 Sequence
AX14796 Sequence
AX14791 Sequence
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AX14799 Sequence
AX14786 Sequence
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AB023806 Gallus ga
AF224120 Gallus ga
U88832 Human grouc
AC002997 Human DNA
AC105178 Homo sapi
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1041)
Vogell,G., Wood,L.S., Parodi,L.A., Hiebsch,R.R., Lind,P.,
Slightom,J., Schellin,K.A., Kaytes,P.S., Bannigan,C.M., Ruff,V.,
Selitt,T and Huff,R.M.
Novel g protein-coupled receptors
Patent: WO 0136473-A 79 25-MAY-2001;
PHARMACIA & UPJOHN COMPANY (US)
  Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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Sequence 79 from Patent W00136473.
AX147834 GI:14346838
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/organism="Homo sapiens"
/db_xref="taxon:9606"
a 294 c 278 g 26
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ACO02997
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KEYWORDS
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AUTHORS
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AX147834
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        GenCore version
Copyright (c) 1993 - 2002
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Maximum DB seq length: 200000000
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ç P	1 ATGTACAACGGGTCGTGCTGCCGCATCGAGGGGACACCATCTCCCAGGTGATGCCGCCG 60	AX148182
Oy Op	61 CTGCTCATTGTGGCCTTTGTGCTGGGGCACTAGGCAATGGGGTCGCCCTGTGTGGTTTC 120 	110N SAYURINE 23 110H FACEIL 10N AX148182 N AX148182.1 GI:14347084 DS
Qy Dp	121 TGCTTCCACATGAAGACCTGGAAGCCCAGCACTTTACCTTTTCAATTTGGCCGTGGCT 180 	numan. Homo sapie Eukaryota; Mammalia;
Oy Db	181 GATTICCICCITATGATCTGCCTGCCTTTTCGGACAGACTATTACCTCAGACGTAGACAC 240 	REFERENCE 1 (Dates I LO 1041) AUTHORS Chen, R., Dang, H.T. and Lowitz, K.P. TITLE Endogenous and non-endogenous versions of human g protein-coupled receptors TOTIONAL PRESENCE.
oy Db	241 TGGGCTTTTGGGACATTCCCTGCCGAGTGGGGTTTCACGTTGGCCATGAACAGGGCC 300 	Arena Pharmaceuticals Location/Qua
O.Y Db	301 GGGAGCATCGTGTTCCTTACGGTGGTGGCTGCGGACAGGTATTTCAAAGTGGTCCACCCC 360 	Adb_xref="taxon:9606"   Adb_xref="taxon:9606"   Adb_xref="taxon:9606"   ORIGIN
Oy Dp	361 CACCACGCGGTGAACACTATCTCCACCCGGTGCCGCTGGCTTCGTCTGCACCTGTGG 420 111111111111111111111111111111111111	Query Match 100.0%; Score 1041; DB 6; Length 1041; Best Local Similarity 100.0%; Pred. No. 0; Matches 1041; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy Db	421 GCCCTGGTCATCCTGGGAACAGTGTATCTTTTGCTGGAGAACCATCTCTGCGTGCAAGAG 480 	Oy 1 ATGTACAACGGGTCGTGCTGCCGCATCGAGGGGGACACCATCTCCCAGGTGATGCCGCCG 60
Oy Dp	481 ACGCCCGTCTCCTGTGAGCTTCATCATGGTCGGCCAATGGCTGGC	Qy         61 CTGCTCATTGTGGCTTGGCGCGCACTAGGCAATGGGGTCGCCCTGTGTGGTTTC         120
0 Q	541 TICCAGCIGGAGIICITIAIGCCCCICGGCAICAICTIAITITGCICCIICAAGAIIGII 600 	OY 121 TGCTTCCACATGAAGACCTGGAAGCCCAGCACTGTTACCTTTTCAATTTGGCCGTCGCT 180
oy Db	601 TGGAGCCTGAGGCGAGGCAGCTGGCCAGACAGCCTCGGATGAAGAAGCGACCCGG 660 	Qy 181 GATTICCTCCTFATGATCTGCCTGCCTTTTCGGACAGACTATTACCTCAGACGTAGACAC 240
oy G	661 TTCATCATGGTGGCAATTGTGTTCATCACGTGCTGCCCAGCGTGTCTGCTAGA 720 	Oy 241 TGGGCTTTTGGGGACATTCCCTGCGGGCTCTTCACGTTGGCCATGAACAGGGCC 300
Oy Dp	721 CTCTATTTCCTCTGGACGGTGCCCTCGAGTGCCTGCGATCCCTCTGTCCATGGGGCCCTG 780 	Qy 301 GGGAGCAFCGTGTTCCTTACGGTGGTGCTGCGGACAGGTATTTCAAAGTGGTCCACCCC 360
o d	781 CACATAACCCTCAGCTTCACCTACATGAACAGCATGCTGGATCCCCTGGTGTATTATTTT 840 	QY 361 CACCACGGGGGAACACTATCTCCACCGGGTGGCGCTGGCATCGTCTGCACCTTGG 420
Oy Dp	841 TCAAGCCCTCCTTTCCCAAATTCTACAACAAGCTCAAAATCTGCAGTCTGAAACCCAAG 900 	Qy 421 GCCCTGGTCATCCTGGGAACAGTGTATCTTTTGCTGGAGAACCATCTCTGCGTGCAAGAG 480
Oy Op	901 CAGCCAGGACACTCAAAAACACAAAGGCCGGAAGATGCCAATTTCGAACTCGGTCGC 960 	Qy 481 ACGGCCGTCTCCTGTGACAGCTTCATCATCGGCCCATGGCTGGC
oy B	961 AGGAGTTGCATCAGTGTGGCAAATAGTTTCCAAAGCCAGTCTGATGGCAATGGGATCCC 1020 	Qy 541 TICCAGCIGGAGIICITIAIGCCCCICGGCAICAITAITITIGCICCTICAAGAIIGII 600 

Oy 181 GAT         Db 181 GAT	Qy 241 TGG       Db 241 TGG	Qy 301 GGG   1    Db 301 GGG	Oy 361 CAC   11   Db 361 CAC	Qy 421 GCC           Db 421 GCC	Qy 481 ACG	Qy 541 TTC     1     Db 541 TTC	Qy 601 TGG         Db 601 TGG	Oy 661 TTC.	Oy 781 CAC         Db 781 CAC	Qy 841 TCA   -   Db 841 TCA	Oy 901 CAG         Db 901 CAG	QY 961 AGG      Db 961 AGG	Qy 1021 CAC         Db 1021 CAC	4 110 TION ION N DS	SOURCE ORGANISM H
OY 601 TGGAGCCTGAGGCGGAGGCAGCTGGCCAGACAGGCTCGGATGAAGAAGGCGACCCGG 660	Qy 661 TTCATCATGGTGGTGCAATTGTGTTCATCATGCTACCTGCCCAGCGTGTCTGCTAGA 720 	<pre>Qy 721 CTCTATTTCCTCTGGACGTGCCTCGAGTGCCTGCGATCCCTCTGTCCATGGGGCCCTG 780                                      </pre>	QY 781 CACATAACCCTCAGCTTCACCTACATGAACAGCATGCTGGATCCCCTGGTGTATTATTT 840	Qy 841 TCAAGCCCTCCTTTCCCAAATTCTACAAGCTCAAAATCTGCAGTCTGAAACCCAAG 900 	Qy       901 CAGCCAGGACACTCAAAAACACAAAGGCCGGAAGAGATGCCAATTTCGAACCTCGGTCGC       960         Db       901 CAGCCAGGACACTCAAAAACACACAAAGGCCGGAAGAGATGCCAATTTCGAACCTCGGTCGC       960	Qy       961 AGGAGTTGCATCAGTGTGCCAAATAGTTTCCAAAGCCAGTCTGATGGGAATGGATCCC       1020         Db       961 AGGAGTTGCATCAGTGTGGCAAATAGTTTCCAAAGCCAGTCTGATGGGCAATGGGATCCC       1020	Oy 1021 CACATTGTTGAGTGGCACTGA 1041 	RESULT 3 LOZGS LOZGS AX299705 LOCUS DEFINITION Sequence 1 from Patent W00173029. ACCESSION AX299705 RESION AX299705. GI:17129250 KENSION AX299705.1 GI:17129250	SOURCE human. ORGANISM Homo sapiens Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	REFERENCE 1 (sites) AUTHORS Ye,J.C., Cravchlk,A.C., di Francesco,V.C. and Beasley,E.M. TITLE Isolated human g-protein coupled receptors, nucleic acid molecules encoding human aper proteins, and uses thereof	JOURNAL Patent: WO 0173029-A 1 04-OCT-2001; PE Corporation (NY) (US) FRATURES LOCATION/Qualifiers	SOURCE 1. 1041 /Organism="Homo sapiens" /db_xref="taxon:9606" OPICIN 208 a 294 c 278 g 261 t	Query Match  Query Match  Query Match  Best Local Similarity 100.0%; Pred. No. 0;  Matches 1041; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Qy         1 ATGTACAACGGGTCGTGCTGCTGCTGCGGGGACACCATCTCCCAGGTGATGCCGCCG 60	<pre>Qy 121 TGCTTCCACATGAAGACCTGGAAGCCCAGCACTGTTTACCTTTTCAATTTGGCCGTGGCT 180</pre>

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AF411110 1041 bp DNA linear PRI 01-NOV-2001
Homo sapiens G protein-coupled receptor (GPRB1) gene, complete cds.
AF411110
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Majumder,K., Vernet,C.A., Casman,S.J., Wolenc,A.R., Spaderna,S.K.,
Padigaru,M., Mishnu,V.S., Tchernev,V.T., Spytek,K.A., Li,L.,
Baumgartner,J.C. and Gusev,V.Y.
Novel proteins and nucleic acids encoding same
Patent: WO 0174904-A 1 11-OCT-2001;
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         Lee, D. K., Nguyen, T., Lynch, K.R., Cheng, R., Vanti, W.B., Arkhitko, O., Lewis, T., Evans, J.F., George, S.R. and O'Dowd, B.F.
Discovery and mapping of ten novel G protein-coupled receptor genes Genee 275 (1), 83-91 (2001)
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Lee, D.K., Nguyen, T., Lynch, K.R., Cheng, R., Vanti, W.B., Arkhitko, O., Lewis, T., Evans, J.F., George, S.R. and O'Dowd, B.F.
Lewis, T., Evans, J.F., George, S.R. and O'Dowd, B.F.
Direct Submission
Submitted (17-AUG-2001) Department of Pharmacology, University of Toronto, 8 Taddle Creek Rd. Rm. 4353, Toronto, ont M5S 1A8, Canada Location/Qualifiers
1. 1041
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60 RESULT 6 AX338373 65 LOCUS .	120 DEFINITION ACCESSION VERSION 125 KEYWORDS	180 185	240 REFERENCE AUTHORS 245	300 TITLE JOURNAL 305 FEATURES	CCC 360 SOURCE	420	480 485	540 Db 6 540 Qy 61	600 Db 66 600 Qy 121 605	660 DB 12 660 QY 18	720 Db 186 720 Qy 241 725	780 Db 246 780 Qy 301	840 Db 306 845 QY 361	900 Db 366 900 Qy 421 905	960 Db 426 960 Qy 481	1020 Db 1025 Qy	DD 546 TICCAG QY 601 TGGAGC
1 ATGTACAACGGGTCGTGCTGCCGCATCGAGGGGACACCATCTCCCAGGTGATGCCGCG	61 CTGCTCATTGTGCTTGTGCTGGGCGCACTAGGCAATGGGGTCGCCCTGTGTGTG	121 TGCTTCCACATGAAGACCTGGAAGCCCAGCACTGTTTACCTTTTCAATTTGGCCGTGGCT	181 GATITCTCTCTTATGATCTGCCTGCCTTTTCGGACAGACTATTACCTCAGACGTAGACAC	241 TGGGCTTTTGGGGACATTCCCTGCCGAGTGGGCCTCTTCACGTTGGCCATGAACAGGGCCC	301 GGGAGCATCGTGCTTACGGTGGTGGCTGCGGACAGGTATTTCAAAGTGGTCCACCCC	361 CACCACGCGGTGAACACTATCTCCACCCGGGTGGCGGCTGGCATCGTCTGCACCCTGTGG	421 GCCCTGGTCATCCTGGGAACAGTGTATCTTTTGCTGGAGAACCATCTCTGCGTGCAAGAG 	481 ACGCCGTCTCCTGTGAGAGCTTCATCATGGAGTCGGCCAATGGCTGGC	541 TTCCAGCTGCAGTTCTTATGCCCCTCGGCATCATCTTATTTTGCTCCTTCAAGATTGTT	601 TGGAGCCTGAGGCGGAGGCAGCTGGCCAGACAGGCTCGGATGAAGAAGGCGACCCGG 	661 TTCATCATGGTGGCAATTGTGTTCATCACATGCTACCTGCCCAGGTGTCTGCTAGA	721 CTCTATTTCCTCTGGACGGTGCCCTCGAGTGCCTGCGATCCCTCTGTCCATGGGGCCCTG	781 CACATAACCCTCAGCTTCACCTACATGAACAGCATGCTGGATCCCCTGGTGTATTTTT	841 TCAAGCCCTCCTTTCCCAAATTCTACAAGCTCAAAAATCTGCAGTCTGAAACCCAAG	901 CAGCCAGGACACTCAAAAACACAAAGGCCGGAAGAGATGCCAATTTCGAACCTCGGTCGC	961 AGGAGTTGCATCAGTGTGGCAAATAGTTTCCAAAGCCAGTCTGATGGGCAATGGGAATCCC	1021 CACATTGTTGAGTGGCACTGA 1041 
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                                                                                                                        under, K., Vernet, C.A., Casman, S.J., Wolenc, A.R., Spaderna, S.K., Ilgaru, M., Mishnu, V.S., Tchernev, V.T., Spytek, K.A., Li, L., Li, L., and Gusev, V.Y. Tcherner, J.C. and Gusev, V.Y. Tenerner, J.C. and nucleic acids encoding same entry wo 0.174904-A 3 11-0CT-2001; agen Corporation (43)
                                                                                        aryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
malia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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/db_xref="taxon:9606"
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Ye,J.C. Cravchik,A.C., di Francesco,V.C. and Beasley,E.M Isolated human g-protein coupled receptors, nucleic acid encoding human gpcr proteins, and uses thereof Patent: Wo 0173029-A 3 04-0CT-2001;
PE Corporation (NY) (US)
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Regulation of human hm74-like g protein
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/db_xref="taxon:9606"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 179172)

Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbricks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Benton, J., Blimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bunay, C., Burcell, K. B., Bowie, S., Brieva, M., Erown, E., Brown, M., Bryant, N.P., Buhay, C., Carer, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M. D., Dathorne, S.R., David, R., Davida, M.L., Dayer, H., Davida, M.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J.; Earnhart, C., Edgar, D., Edwards, C.C., Elbaj, C., Esochto, M., Falls, T., Ferraquico, D., Flaggin, M., Ford, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hawes, A., Hernandez, J., Hernandez, J., Hernandez, O., Hodgson, A., Holloway, C., Hollins, B., Homsl, F., Howard, S., Huber, J., Holloway, C., Jacokson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S.,
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                                                                                                                                                                                                                                                                                                      AGGAGTTGCATCAGTGTGGCAAATAGTTTCCAAAGCCAGTCTGATGGGCAATGGGATCCC 1020
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TGGAGCCTGAGGCGGAGCAGCAGCAGCCAGCCAGGCTCGGATGAAGAAGAGCGACCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGGAGCCTGAGGCGGAGCCAGCAGCTGGCCAGGCTCGGATGAAGAAGGCGACCCGG
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                                                                                          TTCCAGCTGGAGTTCTTTATGCCCCTCGGCATCATCTTATTTTGCTCCTTCAAGATTGTT
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AC026331.18 GI:14547388
HTG; HTGS_PHASEL; HTGS_DRAFT; HTGS_FULLTOP.
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Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J.,
Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C.,
Lewis, L., Li, L., Li, L., Lider, C., Litu, J., Liu, W.,
Loulseged, H., Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R.,
Martincz, E., Massy, E., Mawhiney, E., McLeod, M.P., Meador, M.
Martincz, E., Massey, E., Machedi, P., Meador, M.
Morgan, M., Morris, S., Moser, M., Neal, D., Newtson, N.,
Morgan, M., Morris, S., Moser, M., Neal, D., Newtson, N.,
Nguyen, A., Nguyen, N., Nickerson, E., Nwokenkwo, S.,
Oquih, M., Okwunou, G., Oragunye, N., Nickerson, E., Nwokenkwo, S.,
Reery, J., Peters, L., Pickens, R., Primus, E., Pu, L. L.,
Ouiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M.,
Riliz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N.,
Sisson, I., Sodergren, E., Sondike, T., Talfrod, B., Thomas, N.,
Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R.,
Mall, R., Wang, S., Ward Moore, S., Warren, R., Washington, C.,
Watlington, S., Williams, G., Williamson, A., Walerzkk, R., Wooden, S.,
Watlington, S., Williams, G., Williamson, A., Walerzkk, R., Wooden, S.,
Watlington, S., Williams, G., Williamson, A., Walerzkk, R., Wooden, S.,
Wallshed
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Sequencing vector: M13; L08811
Chemistry: Dye-primer Bodipy: 31% of reads
Chemistry: Dye-primer Bodipy: 31% of reads
Chemistry: Dye-terminator B1g Dye: 69% of reads
Assembly program: Phrap; version 0.990229
Consensus quality: 17881b bases at least Q40
Consensus quality: 178676 bases at least Q20
Estimated insert size: 176741; sum-of-contigs estimation
Quality coverage: 0.x in Q20 bases; sqarose-fp estimation
Quality coverage: 9.4x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (22-MAR-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Jun 25, 2001 this sequence version replaced gi:13877178.
Center: Baylor College of Medicine
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160977: contig of 7598 bp in length
161077: gap of unknown length
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Web Site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
Contact: project Information
Center project name: HAQI
Center project name: RPII-507N20
Center clone name: RPII-507N20
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Worley, K.C.
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1078 167351: contig of 6274 bp in length 7352 167451: gap of unknown length 1352 173389: contig of 5938 bp in length 1390 173489: gap of unknown length 1490 17658: contig of 2769 bp in length 1558: gap of unknown length 1559 176378: gap of unknown length 1559 176379: contig of 2814 bp in length 160cation/Quallifiers
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                                                                                                                                                                     /clone="RP11-507N20"
a 39904 c 41184 g 47913
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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15751 GATTICCICCITAIGAICIGCCIGCCITIICGGACAGACIAIIACCICAGACGIAGACAC 15810
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                                                            1 ATGTACAACGGGTCGTGCTGCCGCATCGAGGGGGACACCATCTCCCAGGTGATGCCGCCG
                                                                                                                                                                                                                     15691 TGCTTCCACATGAAGACCTGGAAGCCCAGCACTGTTTACCTTTTCAATTTGGCCGTGGCT
                                                                                                                                                                                                                                                    GATTTCCTCCTTATGATCTGCCTGCTTTTCGGACAGACTATTACCTCAGACGTAGACAC
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Sequencing vector: plasmid; M7789
Sequencing vector: M3; L08821
Chemistry: Dye-primer Bodipy: 8% of reads
Chemistry: Dye-terminator Big Dye: 92% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 208562 bases at least Q40
Consensus quality: 208562 bases at least Q30
Consensus quality: 210152 bases at least Q30
Estimated insert Size: 205209; sum-of-contigs estimation
Quality coverage: 8x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 13 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                             Worley, K.C.
Direct Submission
Submitted (22-MAR-2000) Human Genome Sequencing Center, Department
                                                                          of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA on Sep 30, 2001 this sequence version replaced gi:14861654.
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Contact: hgsc-help@bcm.tmc.edu
------ Project Information
                                                                                                                          Center: Baylor College of Medicine Center code: BCM
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/db_xref="taxon:9606"
/chromosome="12"
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Center clone name: RP11-324E6
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 818)
Vogeli,G., Wood,L.S., Parodi,L.A., Hiebsch,R.R., Lind,P.,
Slightom,J., Schellin,K.A., Kaytes,P.S., Bannigan,C.M., Ruff,V.,
Sejlitz,T. and Huff,R.M.
Novel g protein-coupled receptors
Patent: WO 0136473-A 11 25-MAY-2001;
PHARMACIA & UPJOHN COMPARY (US)
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Sequence 11 from Patent WO0136473.
AX147766
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/db_xref="taxon:9606"
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Conservative 0; Mismatch
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adjunder, K., Vernet, C.A., Casman, S.J., Wolenc, A.R., Spaderna, S.K.,
Padigaru, M., Mishuu, V.S., Tchernev, V.T., Spytek, K.A., Li, L.,
Baumgartner, J.C. and Gusev, V.Y.
                                                                                                                                Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 0;
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/db_xref="taxon:9606"
318 c 295 g 275
                                                         AX338374 1104 bp
Sequence 4 from Patent WO0174904
AX338374
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CACATTGTTGAGTGGCACTGA 16611
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bass 1 to 1092)
Chen.R., Dang, H.T. and Lowitz, K.P.
Endogenous and non-endogenous versions of human g protein-coupled
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 CACCACGCGGTGAACACTATCTCCACCCGGGTGGCGCTGGCATCGTCTGCACCCTGTGG
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Patent: WO 0136471-A 35 25-MAY-2001;
Arena Pharmaceuticals, Inc. (US)
Location/Qualifiers
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Sequence 35 from Patent W00136471.
AX148194 GI:14347090
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/db_xref="taxon:9606"
320 c 273 g 277
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Young/P.E., Augustus,M., Carter,K.C., Ebner,R., Endress,G.,
Horrigan,S., Soppet,D.R. and Weaver,Z.
Cancer gene determination and therapeutic screening using signature
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Nomura,H., Nielsen,B.W. and Matsushima,K.
Nomolcular cloning of cDNAs encoding a LD78 receptor and putative leukocyte chemotactic peptide receptors
Int. Immunol. 5 (10), 1239-1249 (1993)
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llarity 100.0%; Pred. No. 1.6e-05;
Conservative 0; Mismatches 0;
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     Score 32; DB 6; L
Pred. No. 1.7e-05;
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Location/Qualifiers
3.1%; scc. 100.0%; Pred. No. ... 0; Mismatches
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Sequence 6104 from Patent WO0194629.
AX335595
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/db_xref="taxon:9606"
530 c 525 g 520
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Cancer Res. Inst., Kana
13-1 Takaramachi
Kanazawa, Ishikawa 920
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Human mRNA for HM74.
D10923
D10923.1 GI:219866
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artificial sequence.

I (bases 1 to 5).
Vogeli,G., Wood,L.S., Parodi,L.A., Hiebsch,R.R., Lind,P.,
Slightom,J., Schellin,K.A., Kaytes,P.S., Bannigan,C.M., Ruff,V.,
Scilitz,T. and Huff,R.M.
Novel g protein-coupled receptors
Patent: WO 0136473-A 130 25-MAX-2001;
PHARMACIA & UPDONN COMPANY (US)
artificial sequence.

1 (bases 1 to 24)

Vogeli, G., Wood, L.S., Parodi, L.A., Hiebsch, R.R., Lind, P., Slightom, J., Schellin, K.A., Kaytes, P.S., Bannigan, C.M., Ruff, V., Sejlitz, T. and Huff, R.M.
Sejlitz, T. and Huff, R.M.
Povel g protein-coupled receptors
Patent: WO 0136473-A 162 25-WAY-2001;
PHARMACIA & UPJOHN COMPANY (US)
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1 (bases 1 to 52)

Vogeli,G., Wood,L.S., Parodi,L.A., Hiebsch,R.R., Lind,P.,
Slightom,J., Schellin,K.A., Kaytes,P.S., Bannigan,C.M., Ruff,V.,
Sejlitz,T. and Huff,R.M.
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Sequence 130 from Patent WO0136473.
AX147885
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Mismatches
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Sequence 159 from Patent WO0136473.
AX147914
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    /organism="synthetic cc/db_xref="taxon:32630"
    /note="Novel Sequence"

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/db_xref="taxon:32630"
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/Protein_id="BAA01721.1"
/db_xref="G1:219867"
/dc_xref="G1:219867"
/dc_xref="G
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Novel g protein-coupled receptors
Patent: WO 0136473-A 133 25-MAY-2001;
PHARMACIA & UPJOHN COMPANY (US)
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100.0%; Pred. No. 1.6e-05;
ative 0; Mismatches 0;
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/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Novel Sequence"
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100.0%; Pred. No. 0.66;
tive 0; Mismatches
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/db_xref="taxon:9606"
/cell_line="human monocyte"
/cell_type="monocyte"
61. .1224
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Sequence 162 from Patent W00136473.
AX147917
AX147917.1 GI:14346912
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Sequence 133 from Patent W00136473.
AX147888
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/codon_start=1
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                                                                                            /gene="HM74"
61. .1224
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS JOURNAL

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RESULT 17 AX147888 LOCUS

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Gaps

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RESULT 18 AX147917

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BASE COUNT

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receptor.
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AJ300199.1 GI:11558405
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/codon_start=1
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59. .1141
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Pfeffer, K.
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Best Local Similarity 100.
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AJ300198 G::11558403
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synthetic construct
artificial sequence.
1 (bases 1 to 33)
vogeli,C., Wood,L.S., Parodi,L.A., Hiebsch,R.R., Lind,P.,
Slightom,J., Schellin,R.A., Kaytes,P.S., Bannigan,C.M., Ruff,V.,
Sejlitz,T. and Huff,R.M.
Sejlitz,T. and Huff,R.M.
Povel g protein-coupled receptors
Patent: WO 0136473-A 108 25-MAY-2001;
PHARMACIA & UPJOHN COMPANY (US)
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/db_xref="taxon:32630"
/note="Novel Sequence"
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                                                                        /organism="synthetic construct"
/db_xref="taxon:32630"
/note="Novel Sequence"
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100.0%; Pred. No. 0.58;
ative 0; Mismatches (
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Best Local Similarity 100.0%; Pred. No. 2.1;
Novel g protein-coupled receptors
Patent: WO 0136473-A 159 25-MAY-2001;
PHARMACIA & UPJOHN COMPANY (US)
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Sequence 108 from Patent WO0136473.
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Pfeffer, K.
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/translation="mgKSDHFIVINGKNCCVFRDENIAKVLPPVLGLEFVFGLLGNGL
ALWIFCFHLKSWKSSRIFLFNLAVADFLLITCLPFLTDNYVHNWDWRFGGIPCRVMLF
MLAMNRQSBIFLTTVYAVDRYFRVYHPHHFLNKISNRTAAIISCSFWGLTIGLTVHLLL
YTHMATKRANGSAYLCSSFSICYNFWHDAMFLLEFFLPLAIISCSGRIWSLRQRQMD
RHAKIKRANGANVAAIVFILCFLPSVAVRIRFWLLXYNVRNCDIXSSVDLAFFTT
LSFTYMNSMLDPVVYYFSSFSFPNFFSTCINRCLRKXTLGEPDNNRSTSVELTGDPST
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Mus musculus Puma-g gene for putative seven transmembrane spanning
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/protein_id="CAC17790.1"
/db_xref="GI:11558404"
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Schaub, A., Futterer, A. and Pfeffer, K. Putterer, A. and Pfeffer, K. PumA-G, an interferon gamma inducible gene in macrophages is a novel member of the seven transmembrane spanning superfamily
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Direct Submission
Submitted (10-NOV-2000) Pfeffer K., Institute of Medical
Microbiology, Immunology and Hygiene, Technical University of
Munich, Trogerstr. 9, Munich, D-81675, GERMANY
Location/Qualifiers
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Live 0; Mismatches
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/map="5F"
                                                                                                                                               1. .1956
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/strain="c57BL/6"
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/cell_line="ANA-1"
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1909. .1914
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http://www.sanger.ac.uk/HGp/Chri3
RP11-569E4 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/Dacpac/home.htm
VECTOR: pBACG3.6
IMPORTANT: This sequence is not the entire insert of clone RP11-1569E4 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap.
The true left end of clone RP11-122A14 is at 83451 in this sequence. The true right end of clone RP11-141M24 is at 100 in this
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/note="MRA4 repeat: matches 1. .728 of consensus" complement(14281. .14711) /note="match: 055: Em. A0252887"
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70nce-"MERG repeat: matches -65. .864 of consensus"
7013. .3385
7note-"THEIB repeat: matches 1. .364 of consensus"
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//note="MIR repeat: matches 1. 238 of consensus" 5283. 5363. 5963.
//note="9 copies 9 mer aatatttt 67% conserved" 5771. 6098
//note="AluSx repeat: matches 1. 299 of consensus" complement(6378. 6805)
//note="match: GSS: Em.AQ231235"
complement(6378. 6794)
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/note="match: GSS: Em:AQ388399"
9500. 10559
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1341. .1626
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complement(1. .88)
/note="match: GSS: Em:AQ387473"
/note="match: GSS: Em:AQ387473"
   Further information can be found at
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/note="match: GSS: Em:AQ011789"
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/note="match: GSS: Em:AZ516719"
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/note="match: GSS: En:AQ179843"
complement(14350, 14638)
/note="match: GSS: En:BB9417"
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/note="match: GSS: Em.:A618066"
complement(14461. .14614)
/note="match: GSS: Em::B86556"
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1. .83550
/organism="Homo sapiens"
/db_xref="taxon:9606"
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Submitted (22-FEB-2001) Sanger Centre, Hinxton, Cambridgeshire, Callo 15A, UK. E-mail enquiries: hunquery@sanger.ac.uk Clone requests: clonerequesf@sanger.ac.uk magner.ac.uk Clone requests: clonerequesf@sanger.ac.uk

On Feb 27, 2001 this sequence version replaced gi:13121436.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >-

30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP thtp://www.sanger.ac.uk/Producter/
                                                                                                                                                                                                                                                                                                                                                           /UZABLIA CONTROLLE CONTROL
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Human DNA sequence from clone RPI1-569E4 on chromosome 13, complete
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                                                                                                                                                                                                                                                                /product="putative seven transmembrane spanning receptor"
/protein_id="CAC17791.1"
/db_xref="GI:11558406"
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Mashreghi-Mohammadi,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome 13, constructed by the Sanger Centre Chromosome 13
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cell, BAC clone"
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'note-"129/SVJ ES
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                 /gene="Puma-g"
/2404. 4177
                                                                                /gene="Puma-g"
/2462. ٦=**
                                                                                                                                                                    2462. .3544
/gene="Puma-g"
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34618. .35081

/note="L2 repeat: matches 1796. .2267 of consensus" 35137. .35237

/note="L2 repeat: matches 2403. .2491 of consensus" 35203. .35234

/note="l1 copies 2 mer ag 100% conserved" 36855. .37333

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                                                                                                                                                                                                                                                                                                      consensus
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                                            .198 of consensus"
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fnote="80 copies 2 mer tc 68% conserved"
19563. 29844
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complement(39901. 40653)
/note="match: GSs: Em:A0541398"
complement(40197. 40653)
                                   note="MIR repeat: matches 36. 7778, .18088
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria: Primates; Catarrhini; Hominidae: Homo.

Lubases; Ito 12564)

Manualia; Butheria: Primates; Catarrhini; Hominidae: Homo.

Alsbrooks, S. L., Amaratunge, H. C., Are, J. R., Banks, T., Barbaria, J., Bubrooks, S. L., Amaratunge, H. C., Are, J. R., Banks, T., Barbaria, J., Bunton, J., Burket, C., Burcell, K. L., Byrd, N. C., Carron, T.F., Burket, C., Burket, C., Burket, C., Carron, T. C., Carron, Daukret, C., Burket, C., Burket, C., Carron, T. C., Carron, Daukret, C., Burket, C., Davis, C., Carron, T. C., Cayle, M. D., Dathore, S. R., Davis, C., Cleveland, C. D., Cox, C. Coyle, M. D., Dathore, S. R., Davis, C., Hartis, C., Maris, C., Davis, C., Liu, T., Liu, T., Liu, T., Lu, Lu, T., Lucier, R., Lucier, R., Lucier, R., Lucier, M., Martinez, E., Massey, E., Mawhiney, E., Martin, R., Martindale, A., Martis, S., Mossey, E., Mawhiney, E., Martin, R., Race, A., Bayton, R., Russey, E., Mawhiney, E., Martin, R., Race, A., Patch, C., Petery, J., Peters, J., Peters, L., Pet
                                                                                      complement(41575. 41939)
//note="match: GSS: Em:AQ100514"
/ 41931. 42003
//note="Lize repeat: matches 2488. 2570 of consensus"
/ 4045. 42879
//note="match: GSS: Em:AQ748881"
/ 4046. match: GSS: Em:B82390"
/ 4255- 42554
/ /note="11 copies 4 mer gtgt 84% conserved"
/ 42686. 45177
//note="LiPe16 repeat: matches 3689. 6157 of consensus"
/ 4178. 45245
/ 45245
/ 4177 copies 4 mer cctt 98% conserved"
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Homo sapiens chromosome 12 clone RP11-290121, WORKING DRAFT
SEQUENCE, 2 unordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 22; DB 9; Length 83550;
Pred. No. 1.9;
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AC012158.30 GI:17402749
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
                           40677. .40951
/note="match: GSS: Em:AQ543863"
complement(41575. .41939)
/note="match: GSS: Em:AQ349212"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 2.1%; Score 22; DB Best Local Similarity 100.0%; Pred. No. 1.9 Matches 22; Conservative 0; Mismatches
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AC012158/c
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AC011080.3 GI:11024919
HTG; HTGS_PHASE2; HTGS_DRAFT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is
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                                                                                                                                                                                                                                                                      Submitted (21-OCT-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Dec 7, 2001 this sequence version replaced gi:17155006.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chemistry: Dye-primer Bodipy: 2% of reads
Chemistry: Dye-primer Bodipy: 2% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 155117 bases at least Q40
Consensus quality: 155780 bases at least Q30
Consensus quality: 155080 bases at least Q30
Consensus quality: 155080 bases at least Q30
Quality coverage: 0x in Q20 bases; sum-of-contigs estimation
Quality coverage: 8.8x in Q20 bases; sum-of-contigs estimation
Tang, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Mall, R., Usmanl, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wall, R., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Waczyk, R., Wooden, S., Worley, K., Wu, Y., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D., Weinstock, G. and Gibbs, R.
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100.0%; Pred. No. 1.7;
tive 0; Mismatches 0; Indels 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Center: Baylor College of Medicine
Center code: BCM
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/db_xref="taxon:9606"
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                                                                                                                                                                                              2 (bases 1 to 152664)
Worley, K.C.
Direct Submission
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Best Local Similarity
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AL Unpublished

2 ( Dasses 1 to 18375)

RE BAIGATION C., Lander, E., Allen, N., Anderson, M., Re Baltaren B., Intron. L., Boundpaller B., Baldarin, J., Barna, M., Beckerly R., Gogglasharky, L., Boundpaller B., Baldarin, J., Barna, M., Beckerly R., Gogglasharky, L., Boundpaller B., Baldarin, J., Barna, M., Beckerly R., Collymore, A., Coone, A., Castle, A., Colangelo, M., Colliso, S., Collymore, A., Coone, P., Dakrellano, K., Dewar, K., Donning, M., Donnellan, L., Doyle, M., Corne, P., Coone, P., Cardark, A., Markaran, R., Markaran, M., Raratas, A., Rain, L., Raratas, A., Rain, R., Raratas, R., Raratas, R., Raratas, A., Rain, R., Raratas, R., Rarata, R., Raratas, R., Raratas, R., Raratas, R., Raratas, R., Rarata,
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 183735)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens, clone RP11-45K2
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21444 183735: contig of 162292 bp in length.
Location/Qualifiers
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1. .21343
/note="assembly_fragment
clone_end:SP6
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/db_xref="taxon:9606"
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AUTHORS
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                                                                                                                             COMMENT
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Enkaryota, Inc 19960; And 10-Oduola, B., Ali-osman, F. R., Allen, C., Alabrooks, S.L., Amaratunge, H.C., Arej, R., Ayele, M., Banks, T., Barbooks, S.L., Amaratunge, H.C., Arej, R., Ayele, M., Barks, T., Barbooks, J., Bankoot, J., Blange, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowde, S., Bricker, C., Burch, P., Burkett, C., Burch, P., Burkett, C., Burch, R., Barks, T., Barbook, J., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Corten, R., Chen, Z., Chowdhry, I., Christopoulos, C., Corten, R., Chen, Z., Chowdhry, I., Christopoulos, C., Corten, R., Delaney, K., Delade, O., Denn, A.L., Ding, Y., Duth, H. H., Douthwatek, Z., Draper, H., Dugan-Rocha, S., Durbin, K. J., Barnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Farlis, C., Harris, K., Harris, C., Lia, C., Liu, J., Liu, J., Liu, M., Lou, W., Lu, M., Landry, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AC055724 11-JAN-2002 BNA linear HTG 31-JAN-2002 Homo sapiens chromosome 12 clone RP11-985023, *** SEQUENCING IN PROGRESS ***, 27 unordered pieces.
                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                           Length 183735;
                                                                                                                             104 others
                                                                                                                                                                                                                                                           0; Indels
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100.0%; Pred. No. 1.6;
tive 0; Mismatches
                                                                                                  vector_side:right"
56460 a 33977 c 35374 g 57820 t
                     21444. .183735
/note="assembly_fragment
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HTG; HTGS_PHASE1.
                                                                                                                                                                                                                                                                                                           860 AATTCTACAACAAGCTCAAAAT 881
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Best Local Similarity 100.
Matches 22; Conservative
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AUTHORS
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(bases 1 to 199607)

REFERENCE

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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 27 contigs. The true order of the pleces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
Direct Submission
Submitted (18-APR-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77000, USA On Jan 31, 2002 this sequence Version replaced gi:10086369.

Center: Baylor College of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Consensus quality: 173746 bases at least Q40
Consensus quality: 186262 bases at least Q30
Consensus quality: 192992 bases at least Q30
Estimated insert size: 196552; sum-of-contigs estimation
Quality coverage: Ox in Q20 bases; agarcose-fp estimation
Quality coverage: 2.9x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                      chemistry: Dye-primer Bodipy: 50% of reads
Chemistry: Dye-terminator Big Dye: 50% of reads
Assembly program: Phrap; version 0.990329First call to
findPhraphist
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of 5217 bp in length
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of 6180 bp in length
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of 8918 bp in length
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of 8948 bp in length
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of 9004 bp in length
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Contact: hgsc-help@bcm.tmc.edu
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 12414)

S Ohno, I., Matsubara, K. and Okubo, K.
Human osteomodulin gene: intron-exon junctions and chromosomal localization
Published Only in DataBase (1997) In press

E 2 (bases 1 to 12414)

S Ohno, I., Matsubara, K. and Okubo, K.
Direct Submission

L Submitted (05-DEC-1997) Ikko Ohno, Institute for Molecular and Submitted (05-DEC-1997) Ikko Ohno, I. Madada-oka, Sulta, Osaka University, Molecular Genetics; 1-3
Yamada-oka, Sulta, Osaka Gis, Japan
Yemada-oka, Sulta, Osaka Gis, Japan
Yemada-oka, Sulta, Osaka Gis, Japan
Yemada-oka, Sulta, Osaka Catago, Tel. 181-6-879-7992,
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LCSNRLESMPPGLPSSLMYLSLENNSISSIPEKYFDKLPKLHTLRMSHNKLODIPYNI
FNLPNIVELSVGHNKLKGAFYIPRILEHLYLONNEIEKMNLTVMCPSIDPLHYHHLTY
IRVDQNKLKEPISSYIFFCFPHIHTIYYGEGRSTNGOTIOLKTQVFRRFPDDDDESED
HDDPDNAHESPEQEGAEGHFDLHYYENQE
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/protein_id-"BAA23982.1"
/db_xref-"G1:269650.2"
/translation-"MGFLSPITVIFFFFGVKVHCQYETYQWDEDYDQEPDDDYQTGFP
FRQNVDYGVPFHQYTLGCVSECFCPTNFPSSMYCDNRLKTIPNIPMHIQQLYLQFNE
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Homo sapiens
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="9"
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1 (bases 1 to 33)
Vogeli,G., Wood,L.S., Parodi,L.A., Hiebsch,R.R., Lind,P.,
Slightom,J., Schellin,K.A., Kaytes,P.S., Bannigan,C.M., Ruff,V.,
Novel g protein-coupled receptors
Patent: WO 0136473-A 107 25-MAY-2001;
PHARMACIA & UPJOHN COMPANY (US)
Location/Qualifiers
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/organism="synthetic construct"
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/db_xref="taxon:9606"
/chromosome="12"
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/note="Novel Sequence"
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AB009589
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AX147862
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Direct Submission

Submitted (10-JAN-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries:

Hunquery(Banger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jan 11, 2002 this sequence version replaced gi:9210935.

During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality) as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one Mi3 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em; EMBL; Sw; SWISSERROT; Tr:, TERMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 9, constructed by the Sanger Centre Chromosome 9 mapping group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://www.sanger.ac.uk/HGD/Chrg
RP11-77D6 is from the library RPCI-11.1 constructed by the group of
Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IMPORTANT: This sequence is not the entire insert of clone RP11-77D6 It may be shorter because we sequence overlapping sections only once, except for a short overlap. The true right end of clone RP11-77D6 is at 152311 in this sequence. The true left end of clone RP11-1933 is at 123116 in this sequence. The true right end of clone RP11-62C3 is at 2000 in this
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/note="Single clone_region. Assembly confirmed by
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Oryza sativa
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Pred. No. 5.8;
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29058 c 29849 g 50557
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/db_xref="taxon:9606"
/chromosome="9"
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74081. .74116
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100.0%; Pred
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AP003771.1 GI:14517645
(bases 1 to 152341)
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Best Local Similarity 100.
Matches 21; Conservative
                              Ramsay, H.
Direct Submission
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AP003771/c
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                                                                                                                                                                                                                           Direct Submission

Submitted (16-OCT-2000) Sanger Centre, Hinxton, Cambridgeshire,
CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
On Oct 17, 2000 this sequence version replaced gi:10277928.

During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence has been finished according to sequence map criteria
as follows. An attempt is made to resolve all sequencing problems,
annotated human repeat sequence elements (e.g. Alu). Where the
sequence is ambiguous, there is an annotation using the 'unsure'
means.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em., EMBL; Sw., SWISSPROT; Tr., TREMBL; Wp., WORMPEP; Information on the WORWPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromsome 13, constructed by the Sanger Centre Chromosome 13 mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr13
RP11-168G12 is from the library RPC1-11.1 constructed at the foreather details see http://bacpac.med.buffalo.edu/
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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00.0%; Pred. No. 5.9;
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41119 a 29504 c 30427 g 42370 t
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/db_xref="taxon:9606"
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Best Local Similarity 100.0%; Pi
Matches 21; Conservative 0;
                              AL161422.14 GI:10862741
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                                                                                                                      Homo sapiens
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AL137848/c
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AC024933/c
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                                                                                                                                                                                                            Clone: Productor

Published Only in DataBase (2001) In press

2 (bases 1 to 175644)

83 Sasaki.T. Matsumoto.T. and Yamamoto.K.

Direct Submission

Submitted (20-JUN-2001) Takuji Sasaki, National Institute of
Agrobiological Resources, Rice Genome Research Program; Kannondal
2-1-2. Tsukuba, Ibaraki 305-8602, Japan

(E-mail:tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/,
Tel:81-298-38-7441, Fax:81-298-38-7468)

NOTE: It currently consists of I contigs caps between the contigs
are represented as runs of N. The order of the pieces is believed
to be correct as given, however the sizes of the gaps between them
are based on estimates that have provided by the submitter. This
sequence will be replaced by the finished sequence as soon as it is
available and the accession number will be preserved.

* This sequence will be replaced

* This sequen
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Stone, N.E., Schmutz, J.J., Shang, J., Pennacchio, L.A., Cox, D.R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheris Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 19538) Stone, N.E., Schmutz, J.J., Shang, J., Pennacchio, L.A., Cox, D.R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (02-NOV-1999) Department of Genetics, Stanford Human Genome Center, 4005 Miranda Avenue, Palo Alto, CA 94304, USA On Nov 2, 1999 this sequence version replaced 91:5757494.
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Homo sapiens chromosome 4 clone C0494Hll, complete sequence.
AC006499
                                                                                                 1 (sites)
Sasaki,T., Matsumoto,T. and Yamamoto,K.
Oryza sativa nipponbare(GA3) genomic DNA, chromosome 6, PAC clone:P0622F03
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Stone, N.E., Schmutz, J.J., Cox, D.R. and Myers, R.M.
Direct Submission
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46662 a 41378 c 40541 g 46713 t
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/cultivar="Nipponbare"
/db_xref="taxon:4530"
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ACO24933 317285 bp DNA linear HTG 06-FEB-2002 Homo sapiens chromosome 3 clone RP11-219D15, WORKING DRAFT SEQUENCE, 27 unordered pieces.
                                                                                                                                                                                                                                                                            /clone="C0494H11"
/clone_lib="ROSWELL PARK CANCER RPCI - 11 Human Male BAC
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Quality: Phrap Quality >=40 99.7% of Sequence;
Estimated Total Number of Errors is 0.6.
STS Content:
STG-86135 G61558
WI-9872 G05448
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
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58996 a 44583 c 41620 g 50185 t
                                                                                                                                                                                                                                    /organism="Homo sapiens"/db_xref="taxon:9606"
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1. .195384
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SHGC-50683 G33721
SHGC-84465 G51855
SHGC-82103 G51922.
                                                                                                            WI-4297 G04613
SHGC-51247 G34292
SHGC4-1530 G01882
                                                                                  SHGC-24200 G33354
SHGC-51172 G34253
                                                                       SHGC-50686 G33724
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length

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artificial sequence.

1 (bases 1 to 20)

Vogell,G., Wood,L.S., Parodi,L.A., Hiebsch,R.R., Lind,P., Slightom,J., Schellin,K.A., Kaytes,P.S., Bannigan,C.M., Ruff,V., Sejlitz,T. and Huff,R.M.
Sejlitz,T. and Huff,R.M.
Povel g protein-coupled receptors
Patent: WO 0136473-A 109 25-MAY-2001;
PHARMACIA & UPJOHN COMPANY (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.0%; Score 21; DB 2; Length 317285; 100.0%; Pred. No. 5.1; tive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                       contig of 5151 bp in length
gap of unknown length
contig of 566 bp in length
gap of unknown length
contig of 6798 bp in length
gap of unknown length
contig of 6910 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   contig of 169654 bp in length
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105193: gap of unknown length
115204: contig of 10011 bp in length
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126830: contig of 11226 bp in length
126930: gap of unknown length
147531: contig of 20601 bp in length
                                                                                                                                                                                                                                                                                                                                                      gap of unknown length contig of 7292 bp in length gap of unknown length contig of 6512 bp in length gap of unknown length
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contig of 8406 bp in length
gap of unknown length
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/organism="synthetic construct"
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of 4865 h
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gap of unknown
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AXI47864
AXI47864.1 GI:14346860
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/db_xref="taxon:9606"
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AX147864
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     MOSEL, M., Neal, D., Newtson, N., Mouyen, M., Mortis, S., Mosel, D., Newtson, S., Oguh, M., Neal, D., Newtson, S., Oguh, M., Neal, D., Newtson, S., Oguh, M., Okwuonu, G., Oragunye, N., Ovledo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Plickens, R., Primus, E., Pul, L.L., Quilles, M., Ren, Y., Rives, M., Rojas, A., Primus, E., Pul, L.L., Quilles, M., Ren, Y., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Sodergren, E., Sonatke, T., Sparks, A., Stanley, H., Stone, H., Stone, H., Stotton, A., Svatek, A., Tamerisa, A., Tamerisa, R., Tang, H., Stutton, A., Svatek, A., Tamerisa, A., Tamerisa, R., Wang, S., Warde, Wor, Y., Walland, D., Vinson, R., Wall, R., Wang, S., Warden, P., Washington, C., Watlington, S., Warden, R., Washington, C., Watlington, S., Warlen, R., Washington, S., Watlington, S., Wallshed
 Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S.,
                                                                                                                                                                                                                                                                                                            Orbital to 317285)
Worley, K.C.
Direct Submission

Direct Submission

Of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Feb 6, 2002 this sequence version replaced gi:15723405.

Center: Baylor College of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Assembly program: Phrap; version 0,990329
Consensus quality: 299405 bases at least Q40
Consensus quality: 30299 bases at least Q30
Consensus quality: 315960 bases at least Q20
Estimated insert size: 325253; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; agarose-fp estimation
Quality coverage: 7.9x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                * NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)

* NOTE: This sequence may represent more than one clone.

* NOTE: This is a "working draft" sequence. It currently

* consists of 27 contigs. The true order of the pieces

* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Sequencing vector: M13;
Chemistry: Dye-terminator Big Dye: 100% of reads
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gap of unknown length
contig of 2035 bp in length
gap of unknown length
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Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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unknown
of 2017 |
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Center clone name: RP11-219D15
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REFERENCE
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TITLE

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Gaps

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2658 others

PAT 08-JUN-2001

linear

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PAT 08-JUN-2001
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Novel g protein-coupled receptors
Patent: WO 0136473-A 160 25-MAY-2001;
PHARMACIA & UPJOHN COMPANY (US)
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synthetic construct
artificial sequence.
1 (bases 1 to 48)
Vogeli,G., Wood,L.S., Parodi,L.A., Hiebsch,R.R., Lind,P.,
Slightom,J., Schellin,K.A., Kaytes,P.S., Bannigan,C.M., Ruff,V.,
Sejlitz,T. and Huff,R.W.
Novel g protein-coupled receptors
Patent: WO 0136473*A 132 25-MAT-2001;
PHARMACIA & UPJOHN COMPANY (US)
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tive 0; Mismatches (
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Pred. No. 95;
; Mismatches
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Sequence 160 from Patent W00136473.
AX147915.1 GI:14346910
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Sequence 132 from Patent W00136473.
AX147887.1 GI:14346882
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/organism="synthetic or
/db_xref="taxon:32630"
/note="Novel Sequence"
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100.0%; Pred. No
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/organism="synthetic c
/db_xref="taxon:32630"
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artificial sequence.
1 (bases 1 to 20)
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Best Local Similarity 100.0
Matches 20; Conservative
   Query Match 1.99
Best Local Similarity 100.0
Matches 20; Conservative
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AX147915/c
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AX147887/c
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artificial sequence.
1 (bases 1 to 2)
Vogeli.G., Wood,L.S., Parodi,L.A., Hiebsch,R.R., Lind,P.,
Slightom,J., Schellin,K.A., Kaytes,P.S., Bannigan,C.M., Ruff,V.,
Sellitz.,T and Huff,R.M.
Novel g protein-coupled receptors
Patent: WO 0136473-A 110 25-MAY-2001;
PHARMACIA & UPJOHN COMPANY (US)
Location/Qualifiers
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synthetic construct
synthetic construct
attificial sequence.
1 (bases 1 to 20)
Vogeli,G., Wood,L.S., Parodi,L.A., Hiebsch,R.R., Lind,P.,
Slightom,J., Schellin,K.A., Kaytes,P.S., Bannigan,C.M., Ruff,V.,
Sajlit,T. and Huff,R.M.
Novel g protein-coupled receptors
Patent: WO 0136473-A 131 25-MAY-2001;
PHARMACIA & UPDOHN COMPANY (US)
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//db_xref-"taxon:32630"
/note-"Novel Sequence"

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    /organism="synthetic construct"
/db_xref="taxon:32630"

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Sequence 110 from Patent W00136473.
AX147865.1 GI:14346861
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Sequence 131 from Patent WO0136473.
AX147886
                 /note="Novel Sequence"
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/ product = frizzled-10"
/product = frizzled-10"
/product = frizzled-10"
/product = frizzled-10"
/product = frizzled-10"
/db_xref = 'GI: 5821259"
/db_xref = 'GI: 5821259"
/db_xref = 'GI: 5821259"
/db_xref = frizzled = fr
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MCKDIGYNWTRMPRUMGHENOREAA.IQLHERAPLVEYGCHGHIKFELCSLYAPWCTBO
MCKDIGYNWTRMPRUMGHENOREAA.IQLHERAPLVEYGCHGHIKFFLCSLYAPWCTBO
MCKDIGYNWTRUDAVLCORAFAEDANGTBO
EPPROSSMLPPWFREPORSTGHDLQOHKDSLSRTSGENDGRFHHVEKAASCAPLCTPG
VDVYWSKDDKQFAVIMIAIWSILCFFSSAFTVLTFLIDPQRFKYPERPIIFLSMCYCV
YSVOYINERSGAESIACDROSGQLYVIGGHERSTGGTIVFLLYYFREAASSLAWVIL
TLTATAAGSKWGHAAIBANSYFHILAAWAIPAVKTIMILVWRRVAGDELTGCYVG
MDVNAALTGFVLIPLACYLIGTSFILGSFVALFHRRVWKTGGENTDKLEKLMVRIG
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Unpublished
2 (bases 1 to 2244)
Stark,M.K., Biggs,J.J., Schoenwolf,G.C. and Rao,M.S.
Direct Submission
Submitted (13-JAN-2000) Neurobiology and Anatomy, University of Utah, 50 N. Medical Dr., Salt Lake City, UT 84132, USA
Location/Qualifiers
/note="Involved in Wnt signaling, encoding a Wnt-7a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 2244)
Stark,M.R., Biggs,J.J., Schoenwolf,G.C. and Rao,M.S.
Characterization of Avian Frizzled Genes in Cranial Placode
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gallus gallus Frizzled-10 (CFz-10) mRNA, complete cds. AF224320 GI:7340131
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428. .2185
//gene="cFz-10"
/note="7-pass transmembrane receptor"
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/organism="Gallus gallus"
/db_xref="taxon:9031"
/dev_stage="stage 4-11 chick"
1. .2244
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/db_xref="G1:7340132"
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Pred. No.
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/product="Frizzled-10"
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100.0%; Pre-
0; }
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Best Local Similarity 100."
Matches 20; Conservative
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
                                                                                                                                                                                                                                                             synthetic construct.
synthetic construct
artificial sequence.
1 (bases 1 to 48)
Vogell,G., Wood,L.S., Parodi,L.A., Hiebsch,R.R., Lind,P.,
Slightom,J., Schellin,K.A., Kaytes,P.S., Bannigan,C.M., Ruff,V.,
Sejlitz,T. and Huff,R.M.
Novel g protein-coupled receptors
Patent: WO 0186473-A 161 25-MAY-2001;
PHARMACIA & UPJOHN COMPANY (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nohno,T.
Identification of chick frizzled-10 expressed in the developing
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Submitted (17-FBB-1999) Tsutcmu Nohno, Kawasaki Medical School,
Molecular Biology: 577 Matsushima, Kurashiki, Okayama 701-0192,
Japan (E-mail:nohno@bcc.kawasaki-m.ac.jp,
Tel:81-86-462-1111(ex.3501), Fax:81-86-462-1199)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kawakami, Y., Wada, N., Nishimatsu, S., Komaguchi, C., Noji, S. and
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Gallus gallus Fz-10 mRNA for Frizzled-10, complete cds
AB023806
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="synthetic construct"
/db_xref="taxon:32630"
/note="Novel Sequence"
15 c 10 g t
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100.0%; Pred. No. 82;
tive 0; Mismatches
                                                                                                                                    DNA
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Sequence 161 from Patent WO0136473.
AXI47916
AXI47916.1 GI:14346911
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/organism="Gallus gallus"
/db_xref="taxon:9031"
/tissue_type="limb_bud"
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/gene="Fz-10"
256. .2013
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Frizzled-10.
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48 GGAGTTGCATCAGTGTGGCA 29
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Nohno, T.
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AB023806/c
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AX147916/C
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VRT 29-MAR-2000

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/translation="MMFPQSRHSGSSHLPQOLKFTTSDSCDRITDEFQLLQAQYHSLK
LECOKLASRESEMQRHYVWYYEMSYGLNIEMHGAGETWRLNGTCAQVLPYLSQEHQQ
QVLCAIERRAKQYTAPELNSTIRQQLQAHQLSQLQALALPLTPLPVGLQPPSLFAVSAG
TGLLSLSALGSQAHLSKEDKNGHDGDTHQEDDGEKSD"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria Primates; Catarrhini; Hominidae: Homo.

[ bases 1 to 37784)
Lamerdin,J.E., McCready,P.M., Adamson,A.W., Burkhart-Schultz,K.,
Garcia,E., Kyle,A., Ramirez,M., Stilwagen,S., Garnes,J.,
Danganan,L., Bruce,R., Quan,G., Montgomery,M., Ow,D., Kobayashi,A.,
Olsen,A.O. and Carrano,A.V.
Sequence analysis of a 1 Mb region in 19q13.1
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31;
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9055. 9117
/gene="AES"
/number=5
9118. 10920
/gene="AES"
/number=5
10921. 10995
/gene="AES"
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/gene="AES"
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10996. .11074
/gene="AES"
/number=6
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11923. .11928
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3347 c 3
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/gene="AES"
/number=2
3144. .6661
/gene="AES"
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6662. .6725
/gene="AES"
/number=3
6726. .8425
/number=3
8426. .8470
/gene="AES"
/gene="AES"
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/number=1
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/gene="AES"
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Matches 20; Conservative
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Hou.E.W. and Li.S.S.-L.

Genomic organization and in situ localization to chromosome 19pl3.3

Genomic organization and ene product exhibiting strong similarity to the amino-terminal domain of Drosophila enhancer of split groucho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Accession Number to human groucho protein encoded by GenBank Accession Number U0441 and to Drosophila melanogaster groucho protein: Swiss Prot Accession Number P16371; the corresponding mRNA sequence is reported in GenBank Accession Numbers X73357 and X73358"
 FSVLYTVPATCVIACYFYERLNMDYWKIVASQOKCKMNNQTKNLDCMMNNSIPAVEIF
WYRIFMLLIVGITSGMWIWTSKTLQSWQNVCSRRLKKRSRRKPASVITSSGIYKKPQH
PQKRHLAKYESTLQPP
173 c 606 9 533 t
                                                                                                                                                                                                                                                                                                    HSGROUCH2 12524 bp DNA linear PRI 05-JAN-1999
Human groucho protein homolog (AES) gene, exons 2-7 and complete
                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein Unpublished (19224)

Hou, E.W. and Li, S.S.-L. Birect Submission (196-FEB-1997) Laboratory of Molecular Genetics, National Institute of Environmental Health Science, Mail Drop D3-05, P.O. Box 12233, Research Triangle Park, NC 27709, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="groucho protein homolog"
join(U88831.1:1. .59,1. .11296)
join(U88831.1:31. .57,3046. .3143,6662. .6725,8426. .8470,9055. .9117,10921. .10995,11075. .11296)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherlai; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 12524)

Miyasaka, H., Choudhury, B.K., Hou, E.W. and Li, S.S.

Molecular cloning and expression of mouse and human cDNA encoding AES and ESG proteins with strong similarity to Drosophila enhancer of split groucho protein.

Eur. J. Blochem. 216 (1), 343-352 (1993)
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join(198831.1:1.57,3046.3143,6662.6725,8426.8470,
9055.3117,10921.10995,11075.>11296)
/gene="AES"
                                                                                                                                             Gaps
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2
                                                                                                     1.9%; Score 20; DB
100.0%; Pred. No. 42;
Live 0; Mismatches
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1. .12524
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HSGROUCH2
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/ rpt__tamily_niu

/ rpt_tamily_niu

complement(28264. .28323)

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/ rame: 1, quality: good, score: 74.000"

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34671.34879
34671.34879
34671.34879
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36861. 36994
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                 .18401)
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complement(34242...
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31373. .31539
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18807. .19120
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on 10463. .10759

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11550. .11683

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2897_.a360
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gion complement(9"Alu"

re complement(4023..3716)
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re complement(4033..4206)
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complement(4600..4830)
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                                                                                                                                                                                                                                                                                                                                             /note="LL19NCO3 library constructed at LLNL from flow-sorted chromosomes from hybrid 5HL2-B, which carries chromosome 19 as its only human chromosome."
2 (bases 1 to 37784)
Lamerdin, J.E.
Direct Submission
Submitted (07-0CT-1997) Human Genome Center, Lawrence Livermore
National Laboratory, 7000 East Ave., Livermore, CA 94551, USA
Map and sequence oriented from centromere to telomere.
R26667 overlaps PAC PC28130 to the left and cosmid F21426 to the right.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /rpt_family="Alu"
6150_.6602
.6602
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7409..7685
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complement(8423..8722)
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                                                                                                                                                              Location/Qualifiers
1. .37784
/organism="Homo sapiens"
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9988. .10088
/note="predicted exon, )
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/rpt_family="Alu"
9164. .9267
/rpt_family="tl"
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Unpublished

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Sharen, Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Blarna, N., Bastlen, V., Boyuslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campoplano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, P., Cohang, D., Calagan, D., Chang, J., Chazaro, B., Ferrelra, P., Fitzhugh, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Goyete, M., Graham, L., Grand Plerre, N., Hagos, B., Heaford, A., Karatas, A., Karla, C., LaRocque, K., Jones, C., Kamat, A., Karatas, A., Kals, C., LaRocque, K., Lamazares, R., Landers, T., Mehoczky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Nail, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Munkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rleback, M., Stantos, R., Schauer, S., Schupback, R., Stantos, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Travis, N., Travis, N., Travis, N., Travis, N., Vola, Y., Wola, N., Vola, N., Willon, T., Wayman, D., Yes, Willey, R., Wola, J., Young, C., Willer, R., Willen, R., Willen, Y., Wayman, D., Yes, Wayman, D., Yes, Willey, R., Salnou, J., Rabodore, J., Willen, R., Wola, N., Yallams, J., Testaye, S., Theodore, J., Ville, R., Wola, N., Wola, N., Wille, R., Wille, R., Willen, R., Wille, R., Wille, R., Wille, R., Willen, R., Wille, R., 
                                                                                                                                                                                                                                                                                                                                                                                                           63400 bp DNA linear HTG 26-DEC-2001
HOMO Sapiens chromosome 8 clone RP11-110116 map 8, LOW-PASS
SEQUENCE SAMPLING.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bass 1 to 63400)
Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo. sapiens chromosome 8, clone RP11-110116
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Center: Whitehead Institute/ MIT Center for Genome Research
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                                                                                                Length 37784;
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However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will
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21510: contig of 695 bp
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22338: contig of 728 bp
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25556: contig of 700 bp
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23136: contig of
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Search completed: October 29, 2002, 04:47:09 Job time : 3464 secs

Query Match
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                     GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
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US-09-356-952-8

US-08-984-709A-49

US-08-73-242-1

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US-08-708-541A-31

US-08-708-541A-33

US-08-708-541A-33

US-08-708-541A-33

US-08-447-411-75

US-08-447-411-75

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US-09-426-998-3

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TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
TITLE OF INVENTION: ENCODING THEM
NUMBER OF SEQUENCE: 37
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 433;
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APPLICATION NUMBER: US/08/664,596B
PCT - US95 - 16766 - 30
US-08 - 952 - 541 - 122
US-08 - 124 - 698 - 122
US-09 - 124 - 698 - 122
US-08 - 496 - 841C - 122
US-08 - 967 - 101 - 73
US-08 - 967 - 101 - 73
US-08 - 952 - 541 - 73
US-08 - 952 - 541 - 73
US-08 - 522 - 541 - 73
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11;
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US-08-496-841C-73
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Best Local Similarity 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Genetics Institute, STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/08664596B Patent No. 5807703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Brown. Scott A.
REGISTRATION NUMBER: 32,724
TELEPHONE: (617) 498-824
TELEPHONE: (617) 498-824
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENTH: 433 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
APPLICANT: Jacobs, Kenneth
APPLICANT: LaVallie, Edward
APPLICANT: Racie, Lisa
APPLICANT: Racie, Lisa
APPLICANT: Treacy, Maurice
APPLICANT: Evans, Cheryl
APPLICANT: Spaulding, Vikki
APPLICANT: Spaulding, Vikki
APPLICANT: Bowman, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Massachusetts
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STATE: Massachus
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: TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
: TITLE OF INVENTION: ENCODING THEM
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massach...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 3380;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.7%; Score 18; DB 1; Length 733;
100.0%; Pred, No. 11;
1ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                 COMPUTER MCSCA.

ZIP: 02140

COMPUTER REDABLE FORM:
MEDULU TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-POS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/738,367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ore 18; DB 2;
ored. No. 12;
Mismatches 0
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION CARACTER CLASSIFICATION: 514
ATTORNEY AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-881
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 733 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 1.7%; Sco
Best Local Similarity 100.0%; P:
Matches 18; Conservative 0;
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Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ), NAME/KEY: CDS
; LOCATION: (13)..(2766)
US-09-156-425-1
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US-09-156-425-1/c
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APPLICANT: McCoy, John
APPLICANT: Lavallie, Edward
APPLICANT: Ratle, Lisa
APPLICANT: Reacy, Maurice
APPLICANT: Treacy, Maurice
APPLICANT: Spaulding, Vikki
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 433;
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ZIP: 02140

MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/738,367
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                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/08738367; Patent No. 5827688; GENERAL INFORMATION:
APPLICANT: MCCOY, John
APPLICANT: LaVallie, Edward
APPLICANT: Racie, Lisa
APPLICANT: Machery, David
APPLICANT: Treacy, Maurice
                                                                                                                                                                                                                                                   Sequence 1, Application US/08738367
Patent No. 5827688
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: BROWN. SCOLE A: 72, 724
REGISTRATION NUMBER: 32, 724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-824
TELEFAX: (617) 498-824
INFORMATION FOR SEQ. ID NO: 1:
SEQUENCE CHARACIENISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             531 TGACATCATGTTCCAGCT 548
                                                                                                                    531 TGACATCATGTTCCAGCT 548
                                                                                                                                    341 TGACATCATGTTCCAGCT 324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 433 base pairs
                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: Massachusetts
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: 11 CONTROL ; MOLECULE TYPE: CDNA US-08-738-367-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Cambridge
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: U ZIP: 02140
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                                                                              18;
                                                                              Matches
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APPLICANT: Margarit, S. M.
APPLICANT: Margarit, S. M.
APPLICANT: Boriack Sjodin, Ann
APPLICANT: Boriack Special
APPLICANT: Boriack Special
APPLICANT: Cole, Philip
APPLICANT: Cole, Philip
TITLE OF INVENTION: A CRYSTAL OF A RAS-SOS COMPLEX AND METHODS OF USE
TITLE OF INVENTION: A CRYSTAL OF A RAS-SOS COMPLEX AND METHODS OF USE
FILE REPERENCE: 600-1-228M CURRENT APPLICATION NUMBER: US/09/356,952
CURRENT APPLICATION NUMBER: US/09/356,952
CURRENT FILING DATE: 1999-07-19
EARLIER FILING DATE: 1999-07-21
NUMBER OF SEO ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Williams, Mark E.
APPLICANT: Stauderman, Kenneth A.
APPLICANT: Stauderman, Kenneth A.
APPLICANT: Stauderman, Kenneth A.
APPLICANT: Harpold, Michael M.
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSE: Heller Ehrman White & McAuliffe
                                                                                                                                                                                                                                                                                                                                          Length 6453;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 3; Length 6453;
12;
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12;
                                                           Ouery Match 1.7%; Score 18; DB Best Local Similarity 100.0%; Pred. No. 12; Matches 18; Conservative 0; Mismatches
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Mismatches
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ilarity 100.0%; Pred. No.
Conservative 0; Mismatc)
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; Sequence 49, Application US/08984709A
; Patent No. 6320032
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 7
US-09-356-952-8/C
'Sequence 8, Application US/09356952
'Patent No. 6117663
'GENERAL INFORMATION:
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        NAME/KEY: CDS
LOCATION: (1664)..(1774)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-356-952-8
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Best Local Similarity
Matches 18; Conserva
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LENGIH: 6453
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                                 Sequence 14, Application US/08306691B
Satent No. 5734039
GENERAL INCEMATION
APPLICANT: Calabreta, Bruno
APPLICANT: Skorski, Tomasz
TITLE OF INVENTION: ANTISENSE
TITLE OF INVENTION: OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES
CORRESPONDENCES: 55
ADDRESSEE: Seldel, Gonda, Lavorgna & Monaco, P.C.
STREET: Two Penn Center, Suite 1800
CITY: Philadelphia
STRATE: Pennsylvania
COUNTRY: Philadelphia
STRATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Monia, Brett P.
APPLICANT: Monia, Brett P.
APPLICANT: Monia, Brett P.
APPLICANT: MAISONING S.
TITLE OF INVENTION: METHODS OF MODULATING TUMOR NECROSIS FACTOR
TITLE OF INVENTION: alpha-INDUCED EXPRESSION OF CELL ADHESION MOLECULES
TITLE OF INVENTION: alpha-INDUCED EXPRESSION OF CELL ADHESION MOLECULES
TITLE OF INVENTION: alpha-1100cob 668A
CURRENT FILING DATE: 1998-12-10
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 10
LENGTH: 6453
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                                                                                                                                                                                                                                                                                                                               ZUP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordferfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/306,691B
FILLING DATE: September 15, 1994
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Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: MONACO, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 331-8
TELEPHONE: (215) 568-8383
TELEPHONE: (215) 568-8383
TELER: NO. 5734039e
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERESTICS:
LENGTH: 6453 base pairs
TYPE: nucleic acid
STARNDEDNESS: SIDGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 10, Application US/09209668A; Patent No. 6114517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 100.0%; P
Matches 18; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: linear
US-08-306-6918-14
RESULT 5
US-08-306-691B-14/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
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US-09-209-668-10/c
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/product= "Streptococcal plasmin receptor"
/evidence= EXPERIMENTAL
/gene= "plr"
/lumber= 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.6%; Score 17; DB 1; Length 1125;
100.0%; Pred. No. 37;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start= 115
/function= "High-affinity binding of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Boyle, Michael D.P.
APPLICANT: Lottenberg, Richard
APPLICANT: Lottenberg, Richard
APPLICANT: Lottenberg, Richard
APPLICANT: Broder, Christopher C.
APPLICANT: Won Mering, Gregory O.
TITLE OF INVENTION: Bacterial Plasmin Receptors as
TITLE OF INVENTION: Fibrinolytic Agents
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS: ADDRESSE: David R. Saliwanchik
STREET: 411 N.W. 41st Street, Suite A-1
              experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Streptococcus pyogenes
STRAIN: M untypable
INDIVIDUAL ISOLATE: 64/14
CLONE: PRL015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence I, Application US/08273247; Patent No. 6136323; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                   TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1125 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: both
TOPPOLOGY: circular
                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  180 TGATTTCCTCCTTATGA 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: mat_peptide
LOCATION: 115..1122
IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     111 TGATTTCCTCCTTATGA 95
  19920810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SATURE.
NAME/KEY: CDS
.....TON: 115..1122
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OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-273-247-1/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 10
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                                                                                                                                                  OPERATING SYSTEM. DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION NUMBER: US/08/984,709A
FILING DATE: 02-DEC-1997
CLASSIFTCATION: 435
ATTORNEY/AGENT INDEMATION: 33,779
REFERENCE/DOCKET NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 33,779
TELECOMMUNICATION NUMBER: 33,779
TELECOMMUNICATION INFORMATION: TELECHOME: (619) 450-8400
TELECAMIONICATION NOW 8EQ ID NO: 49: SEQUENCE CHARACTERISTICS: (19) 450-8400
TELEBANE (619) 587-5360
INFORMATION FOR SEQ ID NO: 49: SEQUENCE CHARACTERISTICS: LENGTH: 789 base pairs TYPE: nucleic acid SYRADEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 1.7%; Score 18; DB 4; Length 7898; Best Local Similarity 100.0%; Pred. No. 12; Matches 18; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/07928462

Patent No. 5328996

GENERAL INFORMATION:
APPLICANT: Boyle, Michael D.P.
APPLICANT: Lottenberg, Richard
APPLICANT: Lottenberg, Richard
APPLICANT: Lottenberg, Richard
APPLICANT: Von Mering, Gregory O.
APPLICANT: Von Mering, Gregory O.
TITLE OF INVENTION: Bacterial Plasmin Receptors as
TITLE OF INVENTION: Pibrinolytic Agents
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSE: David R. Saliwanchik
STREET: 3421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/928,462
4250 Executive Square, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: Coding Sequence
LOCATION: 249...7307
CTHER INFORMATION:
US-08-984-7098-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4009 AGGCGGAGCCAGCTG 3992
                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                610 AGGCGGAGCCAGCTG 627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
                   CITY: La Jolla
STATE: California
                                                                                                                                         COMPUTER: IBM COM
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: UC
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                                                         COUNTRY:
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Sequence 31, Application US/08708541A
Patent No. 5871744
GENERAL INFORMATION:
APPLICANT: VAKHARIA, VIKTAM N.
APPLICANT: WINDT, Egbert
TITLE OF INVENTION: SYNTHETIC RNA TRANSCRIPTS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIKAIDO, MARMELSTEIN, MURRAY & ORAM LLP
STREET: Suite 330 - G Street Lobby
                                                                                                                                                                                                                                                                                                                                                                       DB 4; Length 1935; 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SITEET: Sulte 330 - G SIEGE LODDY
CITY: Washington
STATE: DC
COUNTRY: USA
2IP: 20005-5701
COMPUTER READABLE FORM:
MEDTUM TYPE: Floppy disk
COMPUTER: DEM PC COMPATIBLE
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/708,541A
FILING DATE:
CLASSIFICATION: 424
ATORNEY/AGENT INFORMATION:
NAME: KITTS, Monica C.
REGISTRATION NUMBER: 36,105
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: 202/638-5000
            CURRENT APPLICATION NUMBER: US/09/423,890
CURRENT FILING DATE: 2000-03-06
PRIOR APPLICATION NUMBER: USSN 60/078,153
PRIOR FILING DATE: 1998-03-16
PRIOR APLICATION NUMBER: USSN 60/099,165
PRIOR APPLICATION NUMBER: USSN 60/099,165
PRIOR FILING DATE: 1998-09-04
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 5
LENGTH: 1935
                                                                                                                                                                                                                                                                                                                                                                    1.6%; Score 17; DB 100.0%; Pred. No. 38; tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 202/638-4810
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 3264 base pairs
TYPE: nucleic acid
STRANDENNESS: single
TOPOLOGY: circular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              659 GCATGCTGGATCCCCTG 675
CPI-085CPPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                        812 GCATGCTGGATCCCCTG 828
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Best Local Similarity 100.0
Matches 17; Conservative
                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                     , NAME/KEY: CDS
, LOCATION: (25)..(1902)
US-09-423-890-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: CDNA FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: CDS
LOCATION: 97..531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 12
US-08-708-541A-31/c
FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-708-541A-31
                                                                                                                                                                                                                             TYPE: DNA
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US-09-423-890-5
Sequence 5, Application US/09423890
Patent No. 6312934
GENERAL INFORMATION:
APPLICANT: CADUS PHARMACEUTICAL CORPORATION
TITLE OF INVENTION: AND USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               plasmin(ogen)"
/product= "Streptococcal plasmin receptor"
/evidence= EXPERIMENTAL
/gene= "plr"
/number= 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.6%; Score 17; DB 3; Length 1125;
100.0%; Pred. No. 37;
1ve 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    D: experimental
/codon_start= 115
/function="High-affinity binding of
                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/273,247
FILING DATE:
                                                                                                                                                                                             CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/524,411
FILING DATE: 16-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/330,849
FILING DATE: 29-MAR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Sallyanchik, David R.
REGISTRATION NUMBER: 31,794
RECISTRATION NUMBER: 31,794
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELEFEAX: 904-372-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
FRACHENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Streptococcus pyogenes
STRAIN: M untypable
INDIVIDUAL ISOLATE: 64/14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label- PLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEO ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1125 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    180 TGATTTCCTCCTTATGA 196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: 115.1122 IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: mat_peptide
               ZIP: 32606
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: CDS
LOCATION: 115..1122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTHER INFORMATION:
CTHER INFORMATION:
CTHER INFORMATION:
CTHER INFORMATION:
US-08-273-247-1
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OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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Best Local Similarity
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Sequence 33, Application US/08662227

Patent No. 592320

GENERAL INRORMATION:

APPLICANT: VOCEL.

APPLICANT: RECORT, REINHORST

APPLICANT: FRITZINGER, DAVID

TITLE OF INVENTION: RECOMBINANT PROCVF

NUMBER OF SEQUENCES: 39

CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

ADDRESSEE: P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 4138; 39;
                     CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/447,411
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.6%; Score 17; DB 100.0%; Pred. No. 39; ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 1755 S. JEFFERSON DAVIS HIGHWAY CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 07-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5773243man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 1126-101-0
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-220
TELEX: 248655 OPAT UR
INFORMATION FOR SEQ ID NO: 75:
SEQUENCE CHARACTERISTICS:
LENGTH: 4138 Dase pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3149 CAAGCTCAAAATCTGCA 3165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           870 CAAGCTCAAAATCTGCA 886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                        STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3..4001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . LOCATION:
US-08-447-411-75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: VA
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US-08-662-227-33
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                                                                                                                                                                                                                                                                            APPLICANT: VAKHARIA, VIKram N.
APPLICANT: WANDT, Egbert
TITLE OF INVENTION: A METHOD FOR GENERATING BIRNAVIRUS FROM
TITLE OF INVENTION: SYNTHETIC RNA TRANSCRIPTS
CORRESPONDENCE ADDRESS:
Length 3264;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 3264;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA ENCODING COBRA C3, CVF1, AND CVF2
                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: NIKAIDO, MARMELSTEIN, MURRAY & ORAM LLP
STREET: 655 Fifteenth Street, N. W.,
STREET: Suite 330 - G Street Lobby
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION. DATA:
APPLICATION NUMBER: US/08/708,541A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
38;
Score 17; DB 2;
Pred. No. 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICALL.

FILING DATE:
CLASSIFICATION: 424
ATTORNEY AGENT INFORMATION:
NAME: KITTS, MONICA C.
REGISTRATION NUMBER: 36,105
REFERENCE/POCKET NUMBER: P8172-6002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/638-5000
TELEPHONE: 202/638-4810
TELEPHONE: 202/638-4810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.6%; Score 17; DB
100.0%; Pred. No. 38;
tive 0; Mismatches
                                            Mismatches
1.6%; Score 17;
100.0%; Pred. No.
tive 0; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-447-411-75
Sequence 75, Application US/08447411
Patent No. 5773243
GENERAL INFORMATION:
APPLICANT: PRITZINGER, DAVID C.
APPLICANT: BREDEHORST, REINHARD
APPLICANT: BREDEHORST, REINHARD
TITLE OF INVENTION: DNA ENCODING CC
                                                                                                                                                                               RESULT 13
US-08-708-541A-33/C
US-08-708-541A-33/C
Sequence 33, Application US/08708541A
Patent No. 5871744
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: DC
COUNTRY: USA
ZIP: 20005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 202/638-4810
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 3264 base pairs
TYPE: nucleic acid
STRANDENESS: single
                                                                                                       2506 CCACATGAAGACCTGGA 2490
                                                                                126 CCACATGAAGACCTGGA 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 126 CCACATGAAGACCTGGA 142
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Best Local Similarity 100.(
Matches 17; Conservative
Query Match
Best Local Similarity 100.0
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: CDS
LOCATION: 131..3169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: circular MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: Suite 33 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; LOCATION:
US-08-708-541A-33
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                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/09426998

Patent No. 6358706

GENERAL INFORMATION:
APPLICANT: DUBIN, ADERENNE E.
APPLICANT: TANDARSHEE
APPLICANT: ADVASHREE
APPLICANT: GALINDE, JESSICA Y
APPLICANT: GALINDO, JOSE E
TITLE OF INVENTION: DNA ENCODING HUMAN ALPHAIG T-TYPE CALCIUM
TITLE OF INVENTION: DNA ENCODING HUMAN ALPHAIG T-TYPE CALCIUM
TITLE OF INVENTION: USPANEE
TITLE OF INVENTION: 1999-10-26
CURRENT APPLICANTION NUMBER: US/09/426,998
CURRENT FILING DATE: 1999-10-26
NUMBER OF SEQ ID NOS: 5
SCOTWARE PATENTIN VER: 2.0
SEQ ID NO 3
LENGTH: 6822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: DUBIN, ADRIENNE E.
APPLICANT: PYATI, JARASHREE
APPLICANT: ZHU, JESSICA Y
APPLICANT: ZHU, JESSICA Y
APPLICANT: GALINDE, MARK G
APPLICANT: GALINDO, JOSE E
TITLE OF INVENTION: DNA ENCODING HUMAN ALPHAIG T-TYPE CALCIUM
TITLE OF INVENTION: OR E
TITLE OF INVENTION: ONDER: US/09/426,998
CURRENT APPLICATION NUMBER: US/09/426,998
CURRENT FILING DATE: 1999-10-26
NUMBER OF SEQ ID NOS: S
SOFTWARE: PATENTIN VER: 2.0
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                                                                                   Ouery Match 1.6%; Score 17; DB 4; Length 4138; Best Local Similarity 100.0%; Pred. No. 39; Matches 17; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4; Length 6822;
39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.6%; Score 17; DB 100.0%; Pred. No. 39; Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/09426998
Patent No. 6358706
                                                                                                                                                                                                              3149 CAAGCTCAAAATCTGCA 3165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4561 CTGCTCATTGTGGCCTT 4577
                                                                                                                                                                                  870 CAAGCTCAAAATCTGCA 886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 CTGCTCATTGTGGCCTT 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 CTGCTCATTGTGGCCTT 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-09-426-998-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: HOMO SAPIENS
US-09-426-998-4
                       ; MOLECULE TYPE: CDNA US-09-017-947-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 4
LENGTH: 7741
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US-09-426-998-4
                                                                                                                                                                                                                                                                                                    RESULT 17
US-09-426-998-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 4138
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Patent No. 6303754
GENERAL INFORMATION:
APPLICANT: WOCEL, CARL-WILHELM
APPLICANT: BREDEHORST, REINHORST
APPLICANT: RECK, MICHAELL
APPLICANT: RECK, MICHAELL
APPLICANT: RECK, MICHAELL
APPLICANT: FRIZINGER, DAVID
TITLE OF INVENTION: RECOMBINANT PROCVF
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS: 39
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/017,947
Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.6%; Score 17; DB 2;
100.0%; Pred. No. 39;
tive 0; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FLIANS CALLES CALLED TO THE CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/662,227
FILING DATE: 14-JUM-1996
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 1126-0107-0X
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: D.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY
CITY: ARLINGTON
                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/662,227
FILING DATE: 14-JUN-1996
CLASSIFICATION: 530
                                                                                CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 1126-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-2220
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 4138 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 33: SEQUENCE CHARACTER.STICS: LENGTH: 4138 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Db 3149 CAAGCTCAAAATCTGCA 3165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         870 CAAGCTCAAAATCTGCA 886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17; Conservative
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                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: Sing
TOPOLOGY: linear
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
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US-09-017-947-33
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Patent No. 5763173
GENERAL INFORMATION:
APPLICANT: LARRY GOLD
APPLICANT: SUMEDHA JAYASENA
TITLE OF INVENTION: INVIETIOR TITLE OF INVENTION: INVIETIORS TO DNA POLYMERASES
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Swanson and Bratschun, L.L.C.
STREET: 8400 East Prentice Avenue., Suite 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RECISTRATION NUMBER: 33,960
REFERENCE/DOCKET NUMBER: NEX43-1
TELECOMMUNICATION INFORMATION:
  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDENNESS: single
                  TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 10
SEQUENCE CHARACTERISTICS:
LENGTH: 30 Dase pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                 244 GCTTTTGGGGACATTC 259
                                                                                                                                                                                                                                    Query Match 1.5
Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                       2 GCTTTTGGGGACATTC 17
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STATE: Colorado
COUNTRY: IIC>
                                                                                                                                                        ; TOPOLOGY: linear; MOLECULE TYPE: DNA US-08-484-557C-10
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US-08-487-426B-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80111
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                                                             RESULT 19
US-09-487-368A-226/c

Sequence 226, Application US/09487368A

Patent No. 6261840

GENERAL INFORMATION:
APPLICANT: Jacqueline Wyatt

TITLE OF INVENTION: ATS-0093

CURRENT APPLICATION NUMBER: US/09/487,368A

CURRENT FILING DATE: 2000-01-18

NUMBER OF SEQ ID NOS: 240

SEQ ID NO 226

LENGTH: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 10, Application US/08484557C
Patent No. 5693502
GENERAL INFORMATION:
APPLICANT: LARRY GOLD
APPLICANT: SUMEDHA JAYASENA
TITLE OF INVENTION: UNCLEIC ACID LIGAND
TITLE OF INVENTION: INHIBITORS TO DNA POLYMERASES
NUMBER OF SEQUENCES: 74
CORRESPONDENCES: 74
CORRESPONDENCES: SWANSON and Bratschun, L.L.C.
STREET: 8400 East Prentice Avenue., Suite 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb MEDIUM TYPE: Storage

COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WOOZPEECT 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,557C
FLING DATE: 7-JUNE-1995
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 0/7/14,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION NUMBER: 0/7/36,428
FILING DATE: 11-JUNE-1990
PRIOR APPLICATION NUMBER: 0/7/36,428
FILING DATE: 11-JUNE-1990
PRIOR APPLICATION NUMBER: 0/7/36,428
FILING DATE: 1-JUNE-1990
PRIOR APPLICATION NUMBER: 0/7/536,428
FILING DATE: 1-GUNE-1990
PRIOR APPLICATION NUMBER: 0/7/546,624
FILING DATE: 21-GCTOBER: 1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Antisense Oligonucleotide US-09-487-368A-226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 33,960
REFERENCE/DOCKET NUMBER: NEX43-3
5083 CTGCTCATTGTGGCCTT 5099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   431 TCCTGGGAACAGTGTA 446
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CITY: Denver
STATE: Colorado
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 20
US-08-484-557C-10
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Patent No. 6183967
Patent No. 6183967
Patent No. 6183967
APPLICANT: Jayasena, Sumedha
APPLICANT: GOld, Larry
TITLE OF INVERTION: NUCLeic Acid Ligand Inhibitors to DNA Polymerases
FILE REFERENCE: NEX 43C/PCT-CIP
CURRENT APPLICATION NUMBER: 08709/258,797
CURRENT FILING DATE: 1999-03-01
EARLIER APPLICATION NUMBER: 08/945,734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                        APPLICANT: LARRY GOLD
APPLICANT: SUMEDHA JAYASENA
TITLE OF INVENTION: NUCLEIC ACID LICANDS
TITLE OF INVENTION: THAT BIND TO AND INHIBIT DNA
TITLE OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 3; Ler
1.1e+02;
thes 0;
                                                                                                                                                                                                                                                                         E: Swanson and Bratschun, L.L.C.
8400 East Prentice Avenue.,Suite 200
                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 1.5%; Score 16; DB Best Local Similarity 100.0%; Pred. No. 1.1 Matches 16; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: PCT/US96/09451
FILING DATE: 05-JUNE-1996
APPLICATION NUMBER: 08/487,426
FILING DATE: 7-JUNE-1995
PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/487,720
PRIOR APPLICATION DATA: 7-JUNE-1995
APPLICATION NUMBER: 08/484,557
APPLICATION NUMBER: 08/484,557
ATTONNEY/AGENT INFORMATION:
NAME: BAITY J. SWANSON
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: 33,215
REFERENCE/DOCKET NUMBER: 33,215
RELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/945,734 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: MS-DOS
SOFTWARE: WORDPERFECT 6.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 10.
SEQUENCE CHARACTERISTICS:
LENGTH: 78 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     244 GCTTTTGGGGACATTC 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26 GCTTTTGGGGACATTC 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                   Colorado
                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                  ADDRESSEE: Swa
STREET: 8400 E
CITY: Denver
STATE: Colorad
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: 11
MOLECULE TYPE:
      Patent No. 6020130
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1.5%; Score 16; DB 1; Length 30; 100.0%; Pred. No. 1.1e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                       Sequence 10, Application US/08487720A
Patent No. 5874557
GENERAL INPORMATION:
APPLICANT: LARRY GOLD
APPLICANT: SUMEDHA JAYASENA
TITLE OF INVENTION: INHIBITORS TO DNA POLYMERASES
TUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson and Bratschun, L.L.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Swanson and Bratschun, L.L.C.
STREET: 8400 East Prentice Avenue, Suite 200
CITY: Denver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Storage
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
OFBRATING SYSTEM: MS-DOS
OSCHWARE: WOTGPETfect 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,720A
FILING DATE: 7-UNE-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION NUMBER: 07/536,428
FILING DATE: 11-UNE-1990
PRIOR APPLICATION NUMBER: 07/546,624
FILING DATE: 11-UNE-1990
PRIOR APPLICATION NUMBER: 07/536,428
FILING DATE: 11-UNE-1990
APPLICATION NUMBER: 07/546,624
FILING DATE: 21-OCTOBER-1992
ATTONNEY/AGENT INFORMATION:
NAME: Diane Cruz
ATTONNEY/AGENT INFORMATION:
TELECOMMUNICATION NUMBER: 33,960
REFERENCE/DOCKET NUMBER: 31,960
REFERENCE/DOC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 10, Application US/08945734
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                                                                                                                      244 GCTTTTGGGGACATTC 259
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Best Local Similarity 100.
Matches 16; Conservative
                     Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                                                        2 GCTTTTGGGGACATTC 17
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US-08-487-720A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: Colorado
COUNTRY: USA
ZIP: 80111
                                                                                                                                                                                                                                                                                                  US-08-487-720A-10
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US-08-945-734-10
   Query Match
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US-09-06-756-386

US-09-06-756-386

Sequence 386, Application US/09060756

Patent No. 6183957

GENERAL INFORMATION:

APPLICANT: Cole, Stewart

APPLICANT: Gordon, Stephen

APPLICANT: Billault, Alain

TITLE OF INVENTION: HE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA

TITLE OF INVENTION: LIBRARY APPLICATION TO THE DETECTION OF MYCOBACTERIA

TITLE OF INVENTION: LIBRARY APPLICATION TO THE DETECTION OF MYCOBACTERIA

CURRENT APPLICATON UNMBER: US/09/060,756

CURRENT FILING DATE: 1998-04-16

NUMBER OF SEQ ID NOS: 743

SEQ ID NO 386

LENTH: 287

LENTH: 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Cole, Stewart
APPLICANT: Cole, Stewart
APPLICANT: Buchrieser-Brosch, Roland
APPLICANT: Buchrieser-Brosch, Roland
APPLICANT: Gordon, Stephen
TITLE OF INVENTION: METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM
TITLE OF INVENTION: THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA
TITLE OF INVENTION: LIBRARY APPLICATION TO THE DETECTION OF MYCOBACTERIA
FILE REFERENCE: 3495-0169
CURRENT APPLICATION NUMBER: US/09/060,756
CURRENT APPLICATION NUMBER: US/09/060,756
SURRENT FILING DATE: 1998-04-16
NUMBER OF SEQ ID NOS: 743
SOFTWARE: PATENTIN VET. 2.0
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LOCATION: (various positions within the sequence)
COTHER INFORMATION: applicants are uncertain of bases designated as "n"
US-09-060-756-386
                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                     1.5%; Score 16; DB 5; Length 78; 100.0%; Pred. No. 1.1e+02; Pred. O. Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 511, Application US/09060756; Patent No. 6183957; GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 16; Conservative
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Best Local Similarity 100.
Matches 16; Conservative
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             single
             STRANDEDNESS:
                                         ; TOPOLOGY: lir
; MOLECULE TYPE:
PCT-US96-09451-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-060-756-531
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LENGTH: 99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: Sequence US-09-258-797-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 10, Application PC/TUS9609451
GENERAL INFORMATION:
APPLICANT: LARRY GOLD
APPLICANT: SUMEDHA JAYASENA
TITLE OF INVENTION: NUCLEIC ACID LICAND INHIBITORS TO
TITLE OF INVENTION: DNA POLYMERASES
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSE: SWANSON and Bratschun, L.L.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA

2IP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/09451
FILING DATE: 7-UUNE-1995
FILING DATE: 7-UUNE-1995
PRIOR APPLICATION UMBER: 08/487, 20
FILING DATE: 7-UUNE-1995
PRIOR APPLICATION DATA: 08/487, 20
FILING DATE: 7-UUNE-1995
PRIOR APPLICATION NUMBER: 33, 215
FILING DATE: 7-UUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: BAITY J. SWANSON
FREIERENCE/DOCKET NUMBER: 33, 215
REFERENCE/DOCKET NUMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Swanson and Bratschun, L.L.C.
8400 East Prentice Ave., Suite 200
EARLIER FILING DATE: 1997-10-28
FEARLIER APPLICATION NUMBER: 08/487,426
FEARLIER APPLICATION NUMBER: 08/487,720
FEARLIER FILING DATE: 1995-06-07
FEARLIER FILING DATE: 1995-06-07
FEARLIER FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 119
SEQ ID NO 10
LENGTH: 78
                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Denver
STATE: Colorado
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCT-US96-09451-10
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CITY: San Francisco
CITY: San Francisco
STATE: CA
COUNTRY: US
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATION SYSTEM: PC Compatible
OPERATION SYSTEM: PC COMPATIBLE
OPERATION UNBER: PCTUS95/16766
FILING DATE: 12-DEC-1995
                                                                                                                                                                                                                                                                                                                           Query Match
1.5%; Score 16; DB 4; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.5%; Score 16; DB 5; Length 335; 100.0%; Pred. No. 1.2e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 30
PCT-US95-16766-30/C
Sequence 30, Application PC/TUS9516766
SERRAL INFORMATION:
APPLICANT: COLD SPRING HARBOR, Laboratories
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON
                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: other nucleic acid DESCRIPTION: /desc = "probe" US-08-576-202-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "probe"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 12-DEC-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: ROWLAND, BERTRAM
REGISTRATION NUMBER: 20015
REFREENCE/DOCKET NUMBER: FP6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEPHONE: 415-398-3249
                     TELECOMMUNICATION INFORMATION
TELEPRONE: 415-781-1989
TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                         1007 GGCAATGGGATCCCCA 1022
                                                                                                                                            LENGTH: 335 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 335 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 100.
Matches 16; Conservative
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                                                                                                                                                                                                  RESULT 28
US-09-060-756-46

Sequence 46, Application US/09060756

Batent No. 6183957

GENERAL INFORMATION:
APPLICANT: Cole, Stewart
APPLICANT: Buchirleser-Brosch, Roland
APPLICANT: Buchirleser-Brosch, Roland
TITLE OF INVENTION: LIBRARY APPLICATING A POLYNUCLEOTIDE OF INTEREST FROM
TITLE OF INVENTION: LIBRARY APPLICATION TO THE DETECTION OF MYCOBACTERIA
FILE REFERENCE: 3495-0169
CURRENT APPLICATION NUMBER: US/09/060,756
CURRENT APPLICATION NUMBER: US/09/060,756
NUMBER OF SEQ ID NOS: 743
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. OTHER INFORMATION: applicants are uncertain of bases designated as "n"
US-09-060-756-46
                                                  Gaps
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1.5%; Score 16; DB 4; Length 287; 100.0%; Pred. No. 1.2e+02; tive 0; Mismatches 0; Indels
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100.0%; Pred. No. 1.2e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 30, Application US/08576202
Patent No. 6350576
GENERAL INFORMATION
GENERAL INFORMATION: Migher
APPLICANT: Lisitsyn, Nikolai
TITLE OF INVENTION: CANCER DETECTION PROBES
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
STREET: Four Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURREMY APPLICATION DATA:
APPLICATION NUMBER: US/08/576,202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ROWLEND BETTAM I
REGISTRATION NUMBER: 20015
                                                                                                                    101 ACCCGGGTGGCGGCTG 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           385 ACCCGGGTGGCGGCTG 400
                                                                                            385 ACCCGGGTGGCGCTG 400
                     Best Local Similarity 100.
Matches 16; Conservative
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Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94111
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US-08-576-202-30/c
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ZIP: 94111
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LENGTH: 315
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  Query Match
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Gaps

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Sequence 122, Application US/09124698
Sequence 122, Application US/09124698
Batent No. 6117978
GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBBAULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.5%; Score 16; DB 2; Length 440;
100.0%; Pred. No. 1.2e+02;
ive 0; Mismatches 0; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPOTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/124,698
FILING DATE:
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
RELING APPLICATION DATA:
FILING DATE:
FILING DATE:
         PC-DOS/MS-DOS
n Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: TESTA, HURWITZ & THIBEAULT
High Street Tower - 125 High Street
                             SOFTWARE: Patentin Release #1.0, 'CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,541
                                                                                                                                          ATTORNEY/AGENT INPORMATION:
NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7100
INFORMATION FOR SEQ ID NO: 122:
SEQUENCE CHARACTERISTICS:
LENGTH: 440 base pairs
TYPE: nucleic acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY AGENT INFORMATION:
NAME: Pitcher, Edmund R.
TELECOMUNICATION INFORMATION:
TELEPHONE: (617) 248-7100
INFORMATION FOR SEQ ID NO: 122:
SEQUENCE CHARACTERISTICS:
LENGTH: 440 base pairs
TYPE: nucleic acid
STRANDEDMESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-592-541-122
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Best Local Similarity 100.0
Matches 16; Conservative
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COUNTRY: U.S.A.
ZIP: 02110
                                                                                                   FILING DATE:
CLASSIFICATION: 800
         OPERATING SYSTEM:
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CITY: Boston
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Sequence 122, Application US/08592541
Patent No. 598054
GENERAL INFORMATION:
APPLICANT: ROMBINS, JOHANNA M
APPLICANT: ROMBINS, JOHANNA M
APPLICANT: FRASE, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
CORRESPONDENCE ADDRESS:
US-08-967-101-122
Sequence 122, Application US/08967101
Patent No. 5840540
GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 440;
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                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/967,101
FLING DATE: 10-NOV-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/592,541
FILING DATE:
APPLICATION NUMBER: 08/592,541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.5%; Score 16; DB 2; Lotarity 100.0%; Pred. No. 1.2e+02; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                   ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: High Street Tower - 125 High Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: TESTA, HURWITZ & THIBEAULT
High Street Tower - 125 High Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
TELECOMUNICATION INFORMATION:
TELEPHONE: (617) 248-7100
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 122:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-967-101-122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 440 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 193 ATGATCTGCCTGCCTT 208
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                                                                                                                                                                                                                                                                                                                                       STATE: Massachusetts
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Massachusetts
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Best Local Similarity
Matches 16; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: U.S.A. ZIP: 02110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: High S
CITY: Boston
STATE: Massach
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Sequence 7, Application US/08967101
Petent No. 5840540
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: ST. GENCE-HYSLOP, PETER H
APPLICANT: ST. MONENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES:
NUMBER OF SEQUENCES:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11.5%; Score 16; DB 4; Length 440;
100.0%; Pred. No. 1.2e+02;
tve 0; Mismatches 0; Indels
                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: 05/08/967,101
FILING DATE: 10-NOV-1997
CLASSIFTCATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: TESTA, HURWITZ & THIBEAULT
High Street Tower - 125 High Street
                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/496,841C
FILING DATE: 28-Jun-1995
CLASSIFICATION: GURKNOWN:
ATTORNEY/AGENT INFORMATION:
NAME: Paul F. Fehlner, Ph.D.
RECISTRATION NUMBER: 35,135
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 1.5%; Score 16; DB Best Local Similarity 100.0%; Pred. No. 1.2 Matches 16; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) SEQUENCE DESCRIPTION: SEQ ID NO: 122:
                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (212) 527-7700
TELEFAX: (212) 753-627
INFORMATION FOR SEQ ID NO: 122:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 10-NOV-1997
CLASSIFATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/592,541
                                               STREET: 805 Third Avenue
                                                                                                                                                                              MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 440 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                              ZIP: 10022
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               193 ATGATCTGCCTGCCTT 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        378 ATGATCTGCCTGCCTT 393
                                                                                      STATE: New York COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Massachusetts: U.S.A.
                                                                      CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-496-841C-122
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US-08-967-101-7
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                                               Gaps
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Patent No. 6194153

GENERAL INFORMATION:
APPLICANT: ST GEORGE-HYSLOP, PETER H
APPLICANT: ROWMENS, JOHANNA M
APPLICANT: REASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
CORRESPONDENCES: 183
CORRESPONDENCE ADDRESS:
STREET: High Street Tower - 125 High Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED TO ALZHEIMER'S DISEASE NUMBER OF SEQUENCES: 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 1.5%; Score 16; DB 4; Length 440; Best Local Similarity 100.0%; Pred. No. 1.2e+02; Matches 16; Conservative 0; Mismatches 0; Indels
1.5%; Score 16; DB 3; Length 440;
100.0%; Pred. No. 1.2e+02;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 122, Application US/08496841C
Patent No. 6210919
GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
ROMMENS, JOHANNA M
FRASER, PAUL E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/592,541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/127,480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: PITCHEF, EGMUND R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
INFORMATION FOR SEO ID NO: 122:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA (genomic)
                                                                                      193 ATGATCTGCCTGCCTT 208
                                                                                                              378 ATGATCTGCCTGCCTT 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 440 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         193 ATGATCTGCCTGCCTT 208
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                                             Conservative
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                      Best_Local Similarity
Matches 16; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Boston
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
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US-08-496-841C-122
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US-09-127-480-122
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STATE:
    Query Match
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Gaps

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TYPE: nucleic
STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
             RESULT 38
US-08-592-541-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 73, Application US/08967101
Patent No. 5840540
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMENS, JOHANNA M
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: 10 ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 1.5%; Score 16; DB 2; Length 450; Best Local Similarity 100.0%; Pred. No. 1.2e+02; Matches 16; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                            Length 450;
                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER FEADMBLE FORM:
MEDTUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: Elb PC COMPATIBLE
OPERATIGS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: US/08/967,101
FILING DATE: 10-NOV-1997
CLASSIFICATION 1435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/592,541
FILING DATE:
                                                                                                                                                                                                                          1.5%; Score 16; DB 2; L
100.0%; Pred. No. 1.2e+02;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: Massachusetts
COUNTRY: U.S.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
TELECHANDICATION INFORMATION:
TELEPHONE: (617) 248-7100
INFORMATION FOR SEQ ID NO: 73:
SEQUIENCE CHARACTERISTICS:
LENGTH: 450 base pairs
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: DNA (genomic) US-08-967-101-73
             TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               383 ATGATCTGCCTGCCTT 398
                                                                                         LENGTH: 450 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                        193 ATGATCTGCCTGCCTT 208
                                                                                                                                                                                                                                                                                                                             383 ATGATCTGCCTGCCTT 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           193 ATGATCTGCCTGCCTT 208
                                                                                                                                                                                                                              Query Match 1.5
Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                   ; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-967-101-7
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                                    GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMENS, JOHANNA M
APPLICANT: ROMENS, JOHANNA M
APPLICANT: ROMENS, PAULE
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESS:
ADDRESSE: TESTA, HURWITZ & THIBEAULT
STREET: High Street Tower - 125 High Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 73, Application US/08592541
Patent No. 5986054
GENERAL INFORMATION:
APPLICANT: ST. GENGE-HYSLOP, PETER H
APPLICANT: ST. GENGE-HYSLOP, PETER H
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESS:
ADDRESSES: TESTA, HURWITZ & THIBEAULT
STREET: High Street Tower - 125 High Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 450;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 16; DB 2; I
; Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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100.0%; Pre
0;
; Sequence 7, Application US/08592541
; Patent No. 5986054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . 450 base pairs
nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             193 ATGATCTGCCTGCCTT 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   383 ATGATCTGCCTGCCTT 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: Massachusetts
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                      Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , MOLECULE TYPE: CDNA
US-08-592-541-7
                                                                                                                                                                                                                                                       CLIA.
STATE: MASSAC...
COUNTRY: U.S.A.
TP: 02110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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STREET: his
"mv: Boston
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Gaps

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Sequence 73, Application US/09124698

Patent No. 6117978

GENERAL INFORMATION:
APPLICANT: ST. GENGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: ROMMENS, JOHANNA M
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESS:
ADDRESSEE: HAJA Street Tower - 125 High Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, OCHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 450;
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7. 1.2e+02;
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/124,698
Pred. No. 1.2e+02;
: Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 16; DB 3; Pred. No. 1.26 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/592,541
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-127-480-7; Sequence 7, Application US/09127480
Sequence 7, Application US/09127480
Patent No. 6194153
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPRAN: (617) 248-7000
TELEPRAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.5%; Scillarity 100.0%; P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TOPOLOGY: linear; MOLECULE TYPE: DNA (genomic) US-09-124-698-73
   100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 450 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       193 ATGATCTGCCTGCCTT 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              383 ATGATCTGCCTGCCTT 398
                                                                            383 ATGATCTGCCTGCCTT 398
                                                        193 ATGATCTGCCTGCCTT 208
                     16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                          Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 16; Conserv
   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                             U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Boston
STATE: Massach
COUNTRY: U.S.A
ZIP: 02110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                       RESULT 41
US-09-124-698-73
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                       Matches
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Patent No. 6117978
GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: FRASER, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: QALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESS:
STREET: High Street
CITY: Boston
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o. 1.2e+02; o. Indels
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                                                                                                                                                                                                                                                                                                                                                             Length 450;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/124,698
 Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                 1.5%; Scor.
100.0%; Pred. No. 1....
... 0; Mismatches
                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/592,541
                                               FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEFRAX: (617) 248-700
INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 450 base pairs
TYPE: nucleic acid
STRANDEDNESS: SINGIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGET INFORMATION:
NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 450 base pairs
nucleic acid
EDNESS: single
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                                                                                                                                                                                                                                                                                                                                                         Ouery Match 1.5
Best Local Similarity 100.
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE:
US-09-124-698-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
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                                                                                                                                                                                                                                                                                                                        US-08-592-541-73
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Patent No. 6210919
GENERAL INPORMATION:
GENGE-HYSLOP, PETER H
ROMMENS, JOHANNA M
FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 175
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM:
OPERATING SYSTEM:
OPERATION SYSTEM:
APPLICATION NUMBER: US/08/496,841C
FILING DATE: 28-Jun-1995
CLASSIFICATION: CURROWN>
ATTORNEY/AGENT INFORMATION:
NAME: PAUL F: Fehlner, Ph.D.
REGISTRATION NUMBER: 35,135
TELEPHONE: (212) 753-6237
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 450 base pairs
LENGTH: 450 base pairs
                                                                                                                                                                                                                                    1.5%; Score 16; DB 4; Length 450; 100.0%; Pred. No. 1.2e+02; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 450;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 450 base pairs
LENGTH: 450 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-08-496-841C-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby, & Darby, PC
STREET: 805 Third Avenue
CITY: New York
STATE: New York
            TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 450 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-127-480-73
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                   193 ATGATCTGCCTGCCTT 208
                                                                                                                                                                                                                                                                                                                                          383 ATGATCTGCCTGCCTT 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: New York
COUNTRY: U.S.A.
ZIP: 10022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         193 ATGATCTGCCTGCCTT 208
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Matches 16; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 44
US-08-496-841C-7
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Petent No. 6194153
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL ST. GEORGE-HYSLOP, PETER H
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: O ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 450;
                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/127,480 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.2e+02;
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: High Street Tower - 125 High Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.5%; Score 16; DB 4;
100.0%; Pred. No. 1.2e+0;
tive 0; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: High Street Tower - 125 High Street CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TESTA, HURWITZ & THIBEAULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/592,541
FILING DATE:
ATTORNEY_AGENT INFORMATION:
NAME: Pitcher, Edmund R.
                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/592,541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/127,480 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7100
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 450 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        193 ATGATCTGCCTGCCTT 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               383 ATGATCTGCCTGCCTT 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
                                                        STATE: Massachusetts
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: CDNA
US-09-127-480-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    U.S.A.
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ADDALL
STREET: has
THV: Boston
                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-127-480-73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 43
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REBUILS

1 Sequence 73 Application US/08496841C

1 Sequence 73 Application US/08496841C

2 Sequence 73 Application US/08496841C

3 FREERING APPLICATION CONTRACT OF PETER H

PRESENT PAIL SECONATION OF SEQUENCES AND PROTEINS RELATED

NUMBER OF SEQUENCES: 10 ALLHEIMEN'S DISBABE

CORRESPONDENCE DIDBESS: ADDRESS: ```

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AG114987
AG114987
AG114987
AG114987
GSS, GSS (genome survey sequence).
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Catarrhini; Hominidae; Homo
   Bouilland, F. Study of expressed sequences tags in adipose tissue 1995 Study of expressed sequences tags in adipose tissue 1995 Unpublished (1995) Contact: Frederic Bouilland Centre de Recherche sur l'Endocrinologie moleculaire et l
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Tel: 33 1 45 07 52 87
Fax: 33 1 45 07 58 90
Email: bouillau@infobiogen.fr
automatic cycle sequencing of Pc
putative coding sequence.
Location/Qualiflers
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100.0%; Pre
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100.0%; Pred. No. 0;
ive 0; Mismatches
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                                   ρ
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Gaps

Gaps

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Indels

Length 852;

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TITLE
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KEYWORDS
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   à
  õ
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  Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehikro-chhou, Tsurumi ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-90-505, WE:http://hgp.gsc.riken.go.jp/, Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
   BG677418 852 bp mRNA linear EST 01-MAY-2001 602625245F1 NCI_CGAP_Skn4 Homo sapiens cDNA clone IMAGE:4750187 5',
  ô
   L Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: capabbs-remail.nlh.gov
Tissue Procurement: James Cleaver, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MCC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lnl.gov
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BAC end sequences of Library PTB
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Fullyama.A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
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No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
   Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry of the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM0&t2=PM0-HT0228-181090-001-d08&t3=1999-10-18&t4=1)
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1 (bases 1 to 209)
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1 The FAPESP/LICR Human Cancer Genome Project
Unpublished (1999)
  Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
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MIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. . 10 (11), 1757-1771 (2000) Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara K., and Hayashizaki,Y. Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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GSS: GSS (genome survey sequence).
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Pan troglodytes
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Pan troglodytes
Buc Contagnation (Contagnation of the Contagnation of the C
,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Watahiki,A., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura,T., et al.
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Carninci.p., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
Carninci.p., Shibata,Y., Hayatsu,N., and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
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perpare full-length cDNA libraries for rapid discovery of new
agi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
Hayashizaki,Y.
  Unpublished (2001)
Contact: Yoshihide Hayashizaki
Contact: Yoshihide Hayashizaki
Contact: Yoshihide Hayashizaki
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
The Institute of Physical and Chemical Research (RIKEN)
The Institute of Physical and Chemical Research (RIKEN)
Tel: 81-45-503-9222
Fex: 81-45-503-9216
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   TITLE
  COMMENT
  ORIGIN
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E 1 (bases 1 to 546)

I Unpublished (1999)

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: MGC clome distribution information can be found through the I.M.A.G.E. Consorttim/LLNL at:

High quality sequence stop: 546.

Location/Qualifiers
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Note: this is a NIH_MGC Library."

Note: this is a NIH_MGC Library."
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JOURNAL
COMMENT
   32
  ORGANISM
   REFERENCE
AUTHORS
   AUTHORS
  ACCESSION
   VERSION
KEYWORDS
SOURCE
  REFERENCE
  RESULT 7
BB849390
LOCUS
  ACCESSION
   VERSION
KEYWORDS
   RESULT 6
BG260219
  FEATURES
   SOURCE
```

ð

Gaps

ö

ö

Length 119; Indels

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1...19
/organism="Homo saplens"
/db_xef="texon:9606"
/clone_lib="pr0030"
/dev_stage="Adult"
/note="Organ: pnet; Vector: pucl8; Site_1: Smal; Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196; 716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

13 a 46 c 31 g 29 t
   1.9%; Score 20; DB 9;
100.0%; Pred. No. 31;
tive 0; Mismatches (
      High quality sequence stop: 113.
Location/Qualifiers
   Location/Qualifiers
1. .396
   1.>',
100.0%; Pre
  /note-"Vector:
   AV734147.1 GI:10851692
  136 ACCTGGAAGCCCAGCACTGT 155
   189 CCTTATGATCTGCCTT 208
  24 CCTTATGATCTGCCTGCCTT 43
   110 ACCTGGAAGCCCAGCACTGT 91
   83
C
  Conservative
   Conservative
  Best Local Similarity Matches 20; Conserv
   Local Similarity
es 20; Conserv
  13
  human.
   EST.
   Query Match
   Query Match
  BASE COUNT
   DEFINITION
   ORGANISM
   BASE COUNT
  Best Loca
Matches
  RESULT 10
AV734147
LOCUS
  ACCESSION
VERSION
  TITLE
JOURNAL
  REFERENCE
  AUTHORS
  KEYWORDS
                             FEATURES
  FEATURES
  COMMENT
   ORIGIN
  SOURCE
  ORIGIN
  ò
  g
   ò
   g
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y. Direct Submission

Bulect Submission

Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbeségsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Clones are derived from the chimpanzee BAC library PTB This BAC end clone are derived from the chimpanzee BAC library PTB This BAC end clone tracking errors.
  AW876644 119 bp mRNA linear EST 22-MAY-2000 CM1-PT0030-170100-096-f09 PT0030 Homo sapiens cDNA, mRNA sequence. AW876644 GI:8014819
  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases I to 119)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bordin, S., Costa, F.F., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
  Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=CM1-PT0030-170
100-096-f09&t3=2000-01-17&t4=1)
Seq primer: puc 18 forward
  ö
   Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
   Shotgun sequencing of the human transcriptome with ORF expressed
  Gaps
  ö
  Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
  /cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
| 187 c 157 g 137 t 3 others
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  0; Indels
  1. .665
/organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="PTB-111A21.F"
   100.0%; Preq. ...
  High quality sequence start: 11
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  1002 TGATGGGCAATGGGATCCCCACA 1024
  660 TGATGGGCAATGGGATCCCCACA 638
  : pKS145
   Sequencing: -21M13
   Saci
   /sex="male"
   rel: +55-11-2704922
  Conservative
  Vector
R.Site 1
R.Site 2
   Homo sapiens
   Local Similarity
  PRIMERS
   LIBRARY
  181
  human.
  Query Match
  source
  RESULT 9
AW876644/c
   DEFINITION
ACCESSION
VERSION
  TITLE
JOURNAL
  BASE COUNT
   ORGANISM
   REFERENCE
AUTHORS
   JOURNAL
MEDLINE
COMMENT
  Matches
    AUTHORS
   KEYWORDS
SOURCE
   FEATURES
   TITLE
   COMMENT
   ORIGIN
   rocus
  õ
   g
```

```
Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases I to 396)

Yengy Y., Song, H., Peng, Y., Gu, Y., Gao, G., Xiao, H., Xu, X., Ii, N., Qian, B., Liu, F., Qu, J., Gao, X., Cheng, Z., Xu, Z., Zeng, L., Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Hu, R., Chen, J., Homo sapiens cDNA cdA clones

Unpublished (2000)
     EST 17-OCT-2000
  ö
  Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
Chinese National Human Genome Center at Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
AV734147 AP 396 bp mRNA linear EST 17-OCT-2)
AV734147 cdA Homo sapiens cDNA clone cdAAUC10 5', mRNA sequence.
AV734147
  pTriplEx2; Site_1: sfiIA; Site_2: sfiIB" 53 g 192 t
   Gaps
   ő
   1.9%; Score 20; DB 9; Length 396;
100.0%; Pred. No. 42;
  Indels
   Email: hanzgechgc.sh.cn
This clone is available at CHGC in Shanghai.
  ö
   /tissue_type="pheochromocytoma"
/dev_stage="Adult"
/lab_host="BM25.8"
   Mismatches
  /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="cdAAUC10"
/clone_lib="cdA"
```

```
High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seattle, WA 98109, USA 701 Queen Anne Avenue North, Seattle, WA 98109, USA 701 Queen Anne Avenue North, Seattle, WA 98109, USA 701 G16-3868

Fax: (206) 616-3868

Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC Library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/oxdering_bac.htm) or from Resear h Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu
Plate: 620 row: B column: 23
  /note="Vector: pBACe3.6; Site_1: ECORI; Site_2: ECORI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of ECORI and ECORI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at ECORI sites" 3 others
  528 bp DNA linear GSS 17-JUN-1999
PPCI-11.479K17.TV RPCI-11 Homo sapiens genomic clone RPCI-11.479K17
DNA sequence.
A0537267
A0637267.1 GI:5099902
  and
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 509)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. ar
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 528)
Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter
  Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready Map Building
   Sequence-tagged connectors: A sequence approach to mapping and
  Gaps
   scanning the human genome
Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
99380589
  ö
  /organism="Homo sapiens"
/db_xref="texon:9606"
/clone="plate=650 Col=23 Row=B"
/clone=lib="RPCI-11 Human Male BAC Library"
   1.9%; Score 20; DB 12; Length 509; 100.0%; Pred. No. 45; 0; Mismatches 0; Indels
  Unpublished (1997)
Other_GSSs: RPCI-11-479K17.TJ
Other_GSSs: RPCI-11-479K17.TJ
Ochtect: Shaying Zheo, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
   Contact: Mahairas GG, Wallace JC, Hood L
  High quality sequence stop: 509.
Location/Qualiflers
1. :509
  189 CCTTATGATCTGCCTGCCTT 208
  271 CCTTATGATCTGCCTGCCTT 290
   /sex="male"
  20; Conservative
  Class: BAC ends
   Homo sapiens
   Similarity
   human.
   Query Match
  Best Local
  Source
   DEFINITION
  BASE COUNT
   ORGANISM
  RESULT 13
AQ637267
  JOURNAL
MEDLINE
  Matches
   ACCESSION
  REFERENCE
  JOURNAL
  REFERENCE
  AUTHORS
   VERSION
KEYWORDS
   AUTHORS
   FEATURES
   TITLE
   TITLE
   COMMENT
  COMMENT
  ORIGIN
  SOURCE
   LOCUS
  qq
   ò
   Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui, M.D.
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui, M.D.
Tissue Procurement: W.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CSAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: Location/Qualifiers
   /Anote="Vector: pawpl0; Site_1: Not1; Site_2: EcoRI; 1st strand cDNA was primed with oligo(dT)17 on 50 ng of DNAse-treated, total cellular RNA obtained from 5,000-10,000 mcrodisseted preneoplastic cells histologically-determined to be prostatic intraepithelial neoplasia 2 (PIN2) cells. Double-stranded cDNA was ligated to EcoRI adaptors, 5 cycles of PCR applied to the CDNA with an adaptor-specific primer, and the resulting PCR product subcloned into pawP10 by the UDG-cloning method (Life Technologies). Average insert size is 600 bp. NOTE: Not directionally cloned. This library was constructed by David Krizman."
   AA659324 100-CGAP_Pr2 Homo sapiens cDNA clone IMAGE:1207884 similar to contains Alu repetitive element;, mRNA sequence.
  GSS 13-MAR-1999
   ö
   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 507)

NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

Unpublished (1997)
   Gaps
   AQ401655 509 bp DNA linear GSS 13-MAI HS. S.044_BL_A12_T7 RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=620 Col=23 Row=B, DNA sequence. AQ401655.1 GI:4409993
   ö
   Length 507;
  0; Indels
   1.9%; Score 20; DB 9;
100.0%; Pred. No. 45;
tive 0; Mismatches (
  1..507
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1207884"
/clone=lib="NCI_CGAP_Prz"
/dev_stage="45 years old"
/lab_host="DH108"
  Mismatches
  AA659324
AA659324.1 GI:2595478
   189 CCTTATGATCTGCCTGCCTT 208
  266 CCTTATGATCTGCCTGCCTT 285
   Query Match
Best Local Similarity 100.0
Matches 20; Conservative
   Homo sapiens
   Homo sapiens
  human.
  human.
   source
  DEFINITION
   ORGANISM
  DEFINITION
  BASE COUNT
ORIGIN
   ORGANISM
   AUTHORS
TITLE
   RESULT 12
AQ401655
   ACCESSION
   VERSION
KEYWORDS
SOURCE
   REFERENCE
  JOURNAL
   ACCESSION
   KEYWORDS
SOURCE
                          RESULT 11
   AA659324
  FEATURES
   ò
   g
```

```
505 ATTGTGGCCTTTGTGCTGGG 486
  AA220849.1 GI:1838669
  86
  67 ATTGTGCCTTTGTGCTGGG
   Query Match 1.99
Best Local Similarity 100.6
Matches 20; Conservative
  Mus musculus
  house mouse.
  MGI:406145
  LOCUS
   source
   BASE COUNT
ORIGIN
   ORGANISM
  RESULT 15
AA220849
  TITLE
JOURNAL
  VERSION
KEYWORDS
SOURCE
   REFERENCE
   AUTHORS
   ACCESSION
   FEATURES
  COMMENT
  ò
  Email: est@watson.wustl.edu

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: Xenopus clones from this library are available
through the I.M.A.G.E. Consortium/LLNL at: Info@lmage.llnl.gov

Possible reversed clone: similarity on wrong strand

High quality sequence stop: 323.

Location/Qualifiers
  Menopodinae; Xenopus:

1 (bases 1 to 544)

2 (bases 1 to 544)

2 (bases 1 to 544)

3 (bases 1 to 544)

4 (bases 1 to 544)

4 (bases 1 to 544)

5 (bases 1 to 544)

6 (
   daf73b11.yl NICHD XGC Eyel Xenopus laevis cDNA clone IMAGE:4755429 5' similar to TR:006744 Q06744 MHC CLASS II HISTOCOMPATIBILITY BG813280
   ö
  Email: hbeetigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library availability, please contact Pleter de Jong
(pleter@deJong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Essarch Genet cs (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
  /cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCII1 Human Male BAC Library"
   Gaps
   4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800
Fax: 314 286 1810
   ö
   Length 528;
  1 others
   0; Indels
Medical Center Dr., Rockville, MD 20850
   / Match 1.9%; Score 20; DB 12; Local Similarity 100.0%; Pred. No. 46; hes 20; Conservative 0; Mismatches 0;
  93 t
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   /organism="Homo sapiens"
/db_xref="GDB:7683808"
/db_xref="taxon:9606"
/clone="RRCI-11-47817"
/clone_lib="RPCI-11"
  Location/Qualifiers
1..528
  140 g
  BG813280.1 GI:14184260
   898 AAGCAGCCAGGACACTCAAA 917
   116 AAGCAGCCAGGACACTCAAA 135
  /sex-"Male"
  African clawed frog.
  156 c
                            301 838 0200
301 838 0208
   Class: BAC ends.
  Xenopus laevis
  Query Match
   source
  RESULT 14
BG813280/c
LOCUS
   source
  BASE COUNT
ORIGIN
   DEFINITION
   ORGANISM
   TITLE
JOURNAL
COMMENT
  Matches
  ACCESSION
  VERSION
KEYWORDS
SOURCE
  REFERENCE
  AUTHORS
   FEATURES
   FEATURES
  à
   g
```

```
/clone_lib="NICHD XGC Eyel"
/clone_lib="NICHD XGC Eyel"
/clone_lib="NICHD XGC Eyel"
/dev_stage="adult"
/lab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_l: NotI;
/site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.3 kb. Constructed by Life
Technologies. Note: This is a Xenopus Gene Collection (XGC)
) library."
   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 64)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Gelsel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and
   ö
   AA220849
mwc60405.rl Soares mouse 3NMEL2 5 Mus musculus CDNA clone
IMAGE:660297 5' similar to qb:x15334_rnal CREATINE KINASE, B CHAIN
(HUMAN); qb:M7419 Mouse creatine kinase B gene, complete cds
  This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
   Gaps
   Waterston, R.
The WashU-HHMI Mouse EST Project
Unpublished (1990)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Faz: 314 286 1810
Email: mouseest@watson.wustl.edu
   ö
  DB 10; Length 544;
46;
   0; Indels
  /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_limAGE:660297"
/clone_lib="Scares mouse 3NMB12 5"
/sex="unknown"
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/dev_stage="12.5dpc total fetus"
/lab_host="DH108"
  Seg primer: -28ml3 rev2 ET from Amersham
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Location/Qualifiers
1. 654
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   1.9%; Score 20;
100.0%; Pred. No.
:ive 0; Mismatch
   92 g
```

```
N AL237908.
AL237908.
AL237908.
AL237908.
AL237908.
AL237908.
GI:7897043.
AL237908.
GI:7897043.
GI:7897043.
GI:7897043.
Tetraodon nigroviridis.
Futarodon nigroviridis.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostel; Euteleostel; Neoteleostel;
Actinopterygii; Neopterygii; Teleostel; Euteleostel; Neoteleostel;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodon.
E 1 (bases 1 to 1016)
S Roest-Crollius, H., Jaillon, O., Dasilya, C., Fizames, C., Fisher, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.
Charaterization and repeat analysis of the compact genome of the
  /Ulydians round Septems / Ulydians round Septems / Ulydians round Septems / Ulydians round Septems / Ulone="INAGE:486774" / Clone="INAGE:486774" / Clone="INEMGC_15" / Ulydians round ro
  CUSUJUKB

1016 bp DNA linear GSS 15-MAY-2000
Tetraodon nigroviridis genome survey sequence T7 end of clone
014H16 of library G from Tetraodon nigroviridis, genomic survey
sequence
BG823067 948 bp mRNA linear EST 22-MAY-2001
602728095F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:4867774 5',
  Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov

Tissue Procurement: Arc.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: NIH Intramural Sequencing Center
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.lih.gov
Plate: LLCM1736 row: m column: 23
High quality Sequence stop: 722.
High quality Sequence stop: 722.
   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 948)
NIH-WGC http://mgc.ncl.nih.gov/.
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   Mismatches
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   Pred. No.
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100.0%; Pre-
  BG823067.1 GI:14170654
  189 CCTTATGATCTGCCTGCCTT 208
   504 CCTTATGATCTGCCTGCCTT 485
   20; Conservative
  mRNA sequence.
   Query Match
Best Local Similarity
   Homo sapiens
   sednence.
   286
   human.
   source
  LOCUS
   VERSION
KEYWORDS
SOURCE
ORGANISM
      LOCUS
DEFINITION
  SOURCE
ORGANISM
   BASE COUNT
ORIGIN
   RESULT 18
CNS03CKB/c
   AUTHORS
TITLE
  JOURNAL
   Matches
   ACCESSION
  REFERENCE
  ACCESSION
  AUTHORS
   REFERENCE
  VERSION
KEYWORDS
   FEATURES
  ð
   g
  ö
   BG823216 879 bp mRNA linear EST 22-MAY-2001 602726580F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:4866283 5',
  ö
   adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo. "
   Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov
    Tissue Procurement: ATCC
    CDNA Library Preparation: Ling Hong/Rubin Laboratory
    CDNA Library Preparation: Ling Hong/Rubin Laboratory
    CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
    DNA Sequencing by: NIH Intramural Sequencing Center
    Clone distribution: MGC clone distribution information can be
    found through the I.M.A.G.E. Consortium/LLNL at:
    http://mage.lnh.gov
    Plate: LLCM1732 row: o column: 20
    High quality sequence stop: 797.
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 11 (bases 1 to 879)
11H-MGC http://mgc.ncl.nih.gov/. National institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
   Gaps
   .;
0
   ö
  1.9%; Score 20; DB 10; Length 879;
100.0%; Pred. No. 52;
.ive 0; Mismatches 0; Indels
  1.9%; Score 20; DB 9; Length 654; 100.0%; Pred. No. 48; tive 0; Mismatches 0; Indels
   136 t
  193 g
   BG823216.1 GI:14170803
   607 CTGAGGGGGAGGCAGCT 626
   189 CCTTATGATCTGCCTGCCTT 208
   504 CCTTATGATCTGCCTGCCTT 485
  10 CTGAGGCGGAGGCAGCT 29
  177 c
   Conservative
   Conservative
  mRNA sequence.
BG823216
   Homo sapiens
   Best Local Similarity
Matches 20; Conserv
   Similarity
  ø
  human.
  Ouer,
Best Local Similar
   Query Match
   Query Match
```

DEFINITION

ACCESSION

VERSION KEYWORDS

ORGANISM

SOURCE

AUTHORS

JOURNAL

REFERENCE

BG823216/c

RESULT 16

a à

ORIGIN

source

FEATURES

ö

Gaps

ö

TITLE

RESULT 17 BG823067/c

à

BASE COUNT

ORIGIN

Gaps

ö

```
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1. (bases 1 to 267)

2. (bases 1 to 267)

3. Konno, H., Alzawa, K., Akahira, S., Akiyama, J., Carninci, P., Endo, T., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Eukunishi, Y., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai J., Kikuchi, N., Kojima, Y., Kodota, K., Kagawa, I., Kai J., Kikuchi, N., Kojima, Y., Kodota, K., Sagawa, I., Kai J., Kikuchi, N., Mitha, Y., Kodota, K., Shibata, Y., Shigemoto, Y., Shitaki, T., Soapae, Y., Subata, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Yanamura, M., Tominaga, N., Takahashi, F., Tatahashi, F., Tatahashi, F., Tatahashi, F., Tatahashi, F., Tatahashi, F., Tatahan, Y., Shibata, Y., Subanta, Y., Suzuki, H., Yasunishi, A., Yasunishi, A., Watanabe, S., Yamamura, T., Yasunishi, A., Yokota, T., Kiki Mouse ESTS (Konno, H., et al. 1999)

AL Unpublished (1999)

Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel. 81-45-503-9216
Email: genome-resegscriken.go.jp,
URE:http://genome-resegscriken.go.jp,
URE:http://genome-sgscriken.go.jp,
Autsuura, S., Carninci, P., Muramatsu, M., Okazaki, Y. and Hayashizaki
   Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998) Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y. Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
   AV237023 RIKEN full-length enriched, 10 day neonate skin Mus musculus CDNA clone 4732417M09 3' similar to 214044 M.musculus mrNA AV237023.
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/clone_lib="RIKEN full-length enriched, 10 day neonate
skin"
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100.0%; Pred. No. 1.1
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Best Local Similarity 100.0°
Matches 19; Conservative
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   house mouse.
Mus musculus
   ಥ
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ORIGIN
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AV237023/c
   TITLE
JOURNAL
COMMENT
   ORGANISM
   ACCESSION
   REFERENCE
   AUTHORS
   VERSION
KEYWORDS
SOURCE
   FEATURES
  δλ
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Rumanial: Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 152)
S zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and Venter,J.C.
Use of BAC End Sequences from CalTech Libraries for Sequence-Ready Map Building
Lupublished (1997)
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0200
   Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
Location/Qualifiers
   AQ426903 15272H23.TF CITBI-E1 Homo saplens genomic clone 2572H23,
   ö
  Email: hbe@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: Mi3.21
Class: BAC ends.
   2 (bases 1 to 1016)
cost-Crollius, W. Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,
Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
Saurin, W. and Weissenbach, J.
   Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
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100.0%; Pred. No. 54;
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   Unpublished
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KEYWORDS
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ORIGIN
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JOURNAL
COMMENT
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  DEFINITION
  REFERENCE
AUTHORS
  AUTHORS
  ACCESSION
   REFERENCE
   AUTHORS
                                  JOURNAL
   REFERENCE
   JOURNAL
  JOURNAL
  FEATURES
   FEATURES
   TITLE
   TITLE
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Gaps

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BEB48821 302 bp mRNA linear EST 26-SEP-2000 uv90b09.yl Soares mouse 3NbMS Mus musculus cDNA clone IMAGE:3414425 5', mRNA sequence.
   AW528562 305 bp mRNA linear EST 06-MAR-2000
UI-R-BT1-ako-g-08-0-UI.81 UI-R-BT1 Rattus norvegicus cDNA clone
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 302)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
  Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:1090237
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  Length 302;
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100.0%; Pred. No. 1.3e+02;
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  Indels
  DB 12; L
. 1.3e+02;
ches 0;
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/clone_lib="Soares mouse 3NbMS"
   1.8%; 5cc. 100.0%; Pred. No. ... 0; Mismatches
11
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Matches 19; Conservative
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Matches 19; Conservative
 78
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Mus musculus
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 57
   79
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LOCUS
DEFINITION
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   BASE COUNT
ORIGIN
   BASE COUNT
ORIGIN
  DEFINITION
  ORGANISM
  RESULT 22
BE848821
   REFERENCE
AUTHORS
   ACCESSION
  VERSION
KEYWORDS
SOURCE
  JOURNAL
   FEATURES
   TITLE
   COMMENT
   δλ
  셤
   ò
  g
  168 bp DNA linear GSS 04-AUG-1998 sapiens genomic Sperm Library D Homo sapiens genomic clone Plate-2267 Col-22 Row-F, DNA sequence. AQ069550.1 GI:3384749
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 268) Mahalaas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
   ö
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   Gaps
  Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
99380589
   ö
  Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
VGI Oueen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3818
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
   Length 267;
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Matches 19; Conservative 0; Mismatches 0;
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ORIGIN
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AQ069550
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AUTHORS
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   FEATURES
  TITLE
  COMMENT
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ò g ö

Gaps

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CDNA Library Preparation: David B. Krizman, Ph.D. CDNA Library Preparation: David B. Krizman, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Dy: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.igov/bbrpy/mage/image.html
Insart Length: 491 Std Error: 0.00
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1 (bases 1 to 378)
1 (bases 1 to 378)
2 Nofer,L., Cui,J. and Burnside,J. An expressed sequence tag database of T-cell-enriched activated chicken splenocytes: sequence analysis of 5251 clones 20318616
20318616
Contact: Joan Burnside
   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 396)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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AA526211.
EST 05-AU SAME SAME SAME SEQUENCE.
AA526211.1 GI:2268280
EST.
   Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Michael
Emmert-Buck, M.D., Ph.D.
   ö
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/lab_nost="E.coll TOP10 F'"
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  Molecular Endocrinology
University of Delaware
40 Townsend Hall, Newark, DE 19717, USA
Tel: 302 831-1345
Fax: 302-831-3341
Email: joan@UDel.Edu, www.chickest.udel.edu
Seq primer: T7
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                                  AI981199.1 GI:5884227
  64 CTCATTGTGGCCTTTGTGC 82
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MEDLINE
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TITLE
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  ö
  Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
  The sequence contained an oligo-dr track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NoLI site and the oligo-dr track served to identify it as a clone from the normalized corpus-striatum library cDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com) The following repetitive
   Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
  Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8260
Fax: 319 335 9565
  Gaps
  ö
  Length 305;
   Indels
   ore 19; DB 9; L4
red. No. 1.3e+02;
Mismatches 0;
UI-R-BT1-ako-g-08-0-UI 3', mRNA sequence.
   /organism="Rattus norvegicus"
  ų
   86
   Email: msoares@blue.weeg.uiowa.edu
   Genome Res. 6 (9), 791-806 (1996) 97044477
   1.8%; Score 19;
100.0%; Pred. No.
:ive 0; Mismatch
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   σ
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Best Local Similarity 100.
Matches 19; Conservative
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   Rattus.
   source
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SOURCE
ORGANISM
  LOCUS
DEFINITION
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  BASE COUNT
                            ACCESSION
VERSION
  REFERENCE
AUTHORS
TITLE
   MEDLINE
COMMENT
  RESULT 24
  JOURNAL
  FEATURES
  g
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3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pr7m3 vector. RNA provided by Dr. Bertrand Jordan. Library went through two rounds of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."
   AI510676 417 bp mRNA linear EST 12-MAR-1999 vx91c07.yl Soares_thymus_2NbMT Mus musculus cDNA clone IMAGE:1282572 5', mRNA sequence.
   BG995639 437 bp mRNA linear EST 13-JUN-2001
PMZ-HT0342-190201-008-b04 HT0342 Homo sapiens CDNA, mRNA sequence.
BG995639
                    ö
  ö
   This read is a RESEQUENCE of a previously sequenced mouse clone. This read has been verified (found to hit its original self in the correct orientation)
Seq primer: -40RP from Gibco
High quality sequence stop: 402.
  Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 417)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
  Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                        Gaps
  Gaps
  ö
                      ö
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                      Indels
Pred. No. 1.4e+02;
; Mismatches 0;
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100.0%; Pred
0; N
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   205 TCCCAAATTCTACAACAAG 187
   422 CCCTGGTCATCCTGGGAAC 440
   287 CCCTGGTCATCCTGGGAAC 269
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Matches 19; Conservative
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  MGI:674372
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AUTHORS
TITLE
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BG995639
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   VERSION
KEYWORDS
SOURCE
  JOURNAL
   FEATURES
   COMMENT
   ORIGIN
   LOCUS
   셤
   g
   ð
   ð
  Wells, K.D.
Mapping of Expressed Sequence Tags from a normalized bovine mammary gland cDNA library
Unpublished (2000)
Contact: Sonstegard TS
USDA, ARS, Beltsville Agricultural Research Center
Bdlg. 200 Rm 2A, Beltsville, MD 20705, USA
Tel: 301 504 8416
Fax: 301 504 8414
  Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.
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   ö
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   /note-wector: pAMP10; mRNA made from invasive ovarian tumor, cDNA made by oligo-dT priming. Non-directionally cloned. Size-selected on agarose gel, average insert size 56:5380-5383.  

109 c 81 g 130 t
  Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
1 (bases 1 to 399)
Sonstegard, T.S., Capuco, A.V., Van Tassell, C.P., Ashwell, M.S. and
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   ;
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Plate: 8 row: D column: 18
Seq primer: ATTTAGGTGACACTATAG.
  Email: tads@lpsi.barc.usda.gov
   81 g
   Location/Qualifiers
Location/Qualifiers
   AGGAAACAGCTATGACCAT
   5
   86
  Ouery Match 1.8%; Sco
Best Local Similarity 100.0%; Pr
Matches 19; Conservative 0;
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  67 CCTTATGATCTGCCTGCCT 85
   states."
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   ACCESSION
VERSION
  REFERENCE
  AUTHORS
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  COMMENT
   ORIGIN
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Evolutionary EST analysis identifies rapidly evolving male
  141 ATGAACAGCATGCTGGATC 123
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  . 88
  Contact: Swanson WJ
   Trypanosoma cruzi.
  Conservative
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Best Local Similarity
Matches 19; Conserve
   sequence.
   GSS.
   source
   source
   VERSION
KEYWORDS
SOURCE
ORGANISM
   BASE COUNT
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MEDLINE
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AUTHORS
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  TITLE
    TITLE
  ORIGIN
  g
   ò
  /note="Organ: head_neck; Vector: puc18; Site_1: Smal; Site_2: Smal; A min1-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under
   Homo saplens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 437)
Dias Neto, E., García Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagal, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G. H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Bruustein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
  ô
  BG642257
441 bp mRNA linear EST 21-JUN-2001
3B5 Drosophila accessory gland pSport1 library Drosophila simulans
   Fax: +55-11-2707001

Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtm12.pl?ti=PM2st2=PM2-HT0342-
190201-008-b04&t3=2001-02-19$t4=1)
Seq primer: puc 18 forward
High quality sequence start: 12
High quality sequence stop: 408.
   Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
   Shotgun sequencing of the human transcriptome with ORF expressed
  Drosophila simulans.
Drosophila simulans.
Brosophila simulans
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Petrygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 441)
Swanson, W.J., Clark, A.G., Waldrip-Dail, H.M., Wolfner, M.F. and Aquadro, C.F.
  Gaps
  ô
   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
  Length 437;
   Indels
  ö
   1.8%; Score 19; DB 10;
100.0%; Pred. No. 1.4e+02;
tive 0; Mismatches 0;
   y conditions."
108 g 108 t
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/clone_lib="HT0342"
  Location/Qualifiers
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BG642257
BG642257.1 GI:14522113
   low stringency
  BG995639.1 GI:14399709
   137 CCTGGAAGCCCAGCACTGT 155
  374 CCTGGAAGCCCAGCACTGT 392
   +55-11-2704922
   Query Match 1.84
Best Local Similarity 100.0
Matches 19; Conservative
   1. .437
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  Simpson, A.J.
  BG642257
   Te]:
   source
  RESULT 29
BG642257/c
  VERSION
KEYWORDS
SOURCE
ORGANISM
   BASE COUNT
ORIGIN
  ORGANISM
  DEFINITION
  JOURNAL
MEDLINE
   REFERENCE
  ACCESSION
   AUTHORS
VERSION
KEYWORDS
SOURCE
  REFERENCE
  AUTHORS
  FEATURES
   TITLE
   COMMENT
  ò
  合
```

```
Email: nelsayed@tigr.org
Clones are derived from the Trypanosoma cruzi CL-Brener BAC library
TC3. For clone availability, please contact Dr. Bjorn Andersson at
Uppsala University (bjorn.andersson@genpat.uu.se).
Seg primer: M13 Rev
Class: BAC ends.
  BH190810 458 bp DNA linear GSS 24-OCT-2001
TC3-39E7.TR TC3 Trypanosoma cruzi genomic clone TC3-39E7, DNA
  ö
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/db_xref="taxon:5693"
/clone="TC3-39E7"
/clone_"TC3-39E7"
/note="Vector: pBeloBACI1; Site_1: Hin dIII; Constructed for Uppsala University by Marie-Christine Le Pasller in
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/clone_lib="Drosophila accessory gland pSport1 library"
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  Gaps
reproductive proteins in Drosophila
Proc. Natl. Acad. Sci. U. S. A. 98 (13), 7375-7379 (2001)
21309955
  Trypanosoma cruzi
Bukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
  ö
  Molecular Biology and Genetics
Cornell University
403 Biotechnology Building, Ithaca, NY 14853-2703, USA
Tel: 607 254 4839
Fax: 607 255 6240
Email: wjs18@cornell.edu.
  Length 441;
  Indels
  /tissue_type="accessory gland"
/cell_type="reproductive"
/dev_stage="adult"
/note="bissected accessory glands"
92 c 116 g 104 t 3
  ö
  Score 19; DB 10; I
Pred. No. 1.4e+02;
  cruzi"
  100.0%; Pred. No. 1.4 tive 0; Mismatches
  /organism="Trypanosoma
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BH190810.1 GI:16358086
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human.
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   ACCESSION
VERSION
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SOURCE
  ORGANISM
   MEDLINE
COMMENT
  ACCESSION
  REFERENCE
   AUTHORS
   JOURNAL
   FEATURES
   TITLE
  ò
  В
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I. (bases 1 to 463)

Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.

Use of a random BAC End Sequence Database for Sequence-Ready Map Building (1998)

Lu Mpublished (1998)

Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838
the laboratory of Denis Le Paslier at the Centre d'Etude du Polymorphisme Humain (CEPH), Paris, France. Briefly, Trypanosoma cruzi (CEPH), Paris, France. Briefly, Trypanosoma cruzi (CEPH) as parisially digested with Hin dIII. High molecular weight fragments were ligated in pabeloBACII digested with Hin dIII. The average insert size is 100 kb. Total clone coverage: approx. 33 x the haploid genome."
   B79552 24-0CT-1998 CIT-HSP Homo sapiens genomic clone 2042N4, DNA sequence.
  ö
  ó
  Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: Mi3 Reverse
Class: BAC ends.
  Gaps
  Gaps
  /cell_type="Sperm"
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  .;
O
  0;
  Ouery Match 1.8%; Score 19; DB 12; Length 458; Best Local Similarity 100.0%; Pred. No. 1.5e+02; Matches 19; Conservative 0; Mismatches 0; Indels
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  1 others
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Pred. No. 1.5e+02;
0; Mismatches 0;
  ų
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  125
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/db_xref="taxon:9606"
  126 9
  /clone_lib="CIT-HSP"
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   1.8%; Scotlarity 100.0%; P: Conservative 0;
   /clone="2042N4"
   611 GGCGGAGGCAGCTGGC 629
  146 GGCGGAGCAGCAGCTGGC 164
  B79552
B79552.1 GI:2866575
  121 c
   HindIII"
  .463
   Homo sapiens
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Best Local Similarity
Matches 19; Conserv
  human.
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ORIGIN
  BASE COUNT
ORIGIN
   LOCUS
DEFINITION
   ORGANISM
  JOURNAL
COMMENT
  Matches
  RESULT 31
B79552/c
  ACCESSION
   REFERENCE
  AUTHORS
   VERSION
KEYWORDS
   FEATURES
   TITLE
  SOURCE
   õ
   a
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AQ682105 480 bp DNA linear GSS 28-JUN-1999 HS_2142_B2_GQ2_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2142 Col=4 Row=N, DNA sequence.
   and
  AW928794 tomato flower buds 8 mm to pre-anthesis, Cornell University Lycopersicon esculentum cDNA clone cTOC3K1 5', mRNA
  Lycopersicon.

1 (bases 1 to 481)
van der Hoeven, R.S., Bezzerides, J.l., Matern, A.L., Holt, I.E., Liang, van der Hoeven, R.S., Graven, M.B., Bowman, C.L., Ahn, S., Ronning, F.,
   ö
   Lycopersico<u>n</u> esculentum
Sukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; eussterids I; Solanales; Solanaceae; Solanum;
   Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
High Throughput Sequencing Center
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3887
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
plate: 2142 frow: N column: 4
Seq primer: Mil Reverse
Class: BAC ends
  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Ammania; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 480)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
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Adb_wref="teaxon:9606"
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   Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
99380589
  Gaps
  ö
   Length 480;
   1 others
   1.8%; Score 19; DB 12; Length 48
100.0%; Pred. No. 1.5e+02;
ative 0; Mismatches 0; Indels
   130 t
   High quality sequence stop: 4
   100 g
   GI:8104189
   AQ682105.1 @I:5258088
   668 TGGTGGTGCCAATTGTGTT 686
   r="male"
   29 TGGTGGTGGCAATTGTGTT 11
   122 c
   .480
  sequence.
AW928794
AW928794.1
  Query Match
Best Local Similarity
Matches 19; Conserv
   127
   tomato.
  REFERENCE
   AUTHORS
```

Gaps ö EST 16-MAR-1998

TITLE JOURNAL

COMMENT

FEATURES

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
I (bases 1 to 496)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
In WashU-HHMI Mouse EST Project
In Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashU-HMI Wouse EST Project
  3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT/T3 vector. NA provided by Dr. Bertrand Jordan. Library went through two rounds of normalization, and was constructed by Bento
   This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
  vx91c07.rl Scares_thymus_2NbMT Mus musculus cDNA clone
IMAGE:1282572 5', mRNA sequence.
   Length 482;
  linear
  Indels
   Query Match 1.8%; Score 19; DB 9; Le
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 19; Conservative 0; Mismatches 0;
  /clone_lib="Soares_thymus_2NbMT"
/sex="male"
  Seq primer: -28m13 rev2 ET from Amersham
  mRNA
   1. .496
/organism="Mus musculus"
/strain="c57BL/6J"
/db.xref="taxon:10090"
/clone="IMAGE:1282572"
   Email: mouseest@watson.wustl.edu
  High quality sequence stop: 491.
Location/Qualifiers
  496 bp
    /clone="IMAGE:610006"
   AA866830.1 GI:2962275
  851 CCTTTCCCAAATTCTACAA 869
   286 CCTTTCCCAAATTCTACAA 304
   Mus musculus
  house mouse
   MGI:674372
   122 a
  AA866830
  AA866830
  source
   RESULT 35
AA866830/c
   DEFINITION
   BASE COUNT
ORIGIN
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JOURNAL
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   REFERENCE
   AUTHORS
   VERSION
KEYWORDS
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  SOURCE
  ð
  /organism="Lycopersicon esculentum"
/cultiva="TA406"
/db_xref="taxon:4081"
/clone="crOc3xi"
/clone=lib="tomato flower buds 8 mm to pre-anthesis,
Cornell University"
/tissue_type="flower"
/dev_stage="buds 8mm-to-preanthesis"
/dev_stage="buds 8mm-to-preanthesis"
/dev_stage="buds 8mm-to-preanthesis"
/dev_stage="buds 8mm-to-preanthesis"
/dot="vector: pBlueScript SK(-); Site_1: EcoRI; Site_2:
/hot="vector: pBlueScript Stoker buds and flowers were
taken from greenhouse plants (4-8 wks old, TA496). They
were immediately frozen in liquid nitrogen and then
size-separated while remaining frozen."
   Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi; Eutheria : Primates; Catarrhini; Hominidae; Homo.

Mammalia: Eutheria: Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 482)

Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,

Chisoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Hawkins
,M., Hultman,M., Rucaba,T., Lacy,M., Le,M., Mardis,E.,
Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J., Trewaskis,E.,

Generation and analysis of 280,000 human expressed sequence tags
Generation ever for the following 
   AA169173 482 bp mRNA linear EST 20-DEC-1996 zp20c12.sl Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:610006 3', mRNA sequence.
  ö
,C.M., Fraser,C.M., Martin,G.B., Giovannoni,J.J. and Tanksley,S.D. Generation of ESTs from tomato flower tissue
  Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seg primer: -40M13 fvd. from Amersham
High quality sequence stop: 404.
  Gaps
  ö
  Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.
  1.8%; Score 19; DB 9; Length 481;
100.0%; Pred. No. 1.5e+02;
iive 0; Mismatches 0; Indels
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/db_xref="taxon:9606"
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   Location/Qualifiers
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AA169173.1 GI:1747749
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Best Local Similarity 100.v
   Unpublished (1999)
Contact: CUGI
   Contact: Wilson RK
  1. .481
  155
   human.
   source
  BASE COUNT
ORIGIN
```

DEFINITION

ACCESSION VERSION KEYWORDS SOURCE

RESULT 34 AA169173

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ORGANISM

REFERENCE AUTHORS TITLE JOURNAL MEDLINE COMMENT

FEATURES

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USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4360
Bmail: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
PCR PRimers
   515 bp DNA linear GSS 15-JUN-2000
BNA sequence.
A2253634
  EST 28-DEC-2001
  1 (bases 1 to 509)
Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T., Casas,B., Waray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett,J.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G., Pertea,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and Keele,J.W.
   /note="Vector: pcMv SPORT6; Site_1: XbaI; Site_2: XhoI; Library made from pooled tissue from marrow, alveolar macrophage, ovary, fetal semitendonosus muscle, and fetal longissimus muscle."
   Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 515)
Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S., Akinret
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
   Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
  ö
  Length 509;
  BM287008 509 bp mRNA linear 527250 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
   Indels
   1.8%; Score 19; DB 10; I 100.0%; Pred. No. 1.5e+02; tive 0; Mismatches 0;
   117 t
   FORWARD: AGGAAACAGCTATGACCAT
BACKRARD: GTTTTCCACTACGACG
Plate: 135 row: J column: 23
Seq primer: ATTTAGGTGACACTATAG.
Location/Qualiflers
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/lab_host="DH10B"
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   BM287008.1 GI:17996034
  AZ253634.1 GI:8566837
  855 TCCCAAATTCTACAACAAG 873
  430 TCCCAAATTCTACAACAAG 412
   Contact: Smith TPL
   144 c
  19; Conservative
   house mouse.
   Best Local Similarity
  Bos taurus
   ø
  BM287008
   115
   COW.
   Query Match
   source
                     BM287008/c
LOCUS
  AZ253634/c
LOCUS
   DEFINITION
  ORGANISM
  ORGANISM
  DEFINITION
   BASE COUNT
  REFERENCE
AUTHORS
  MEDLINE
COMMENT
  Matches
   ACCESSION
  ACCESSION
  REFERENCE
  AUTHORS
RESULT 37
   VERSION
KEYWORDS
  JOURNAL
   RESULT 38
  VERSION
KEYWORDS
SOURCE
   FEATURES
  TITLE
  SOURCE
  ORIGIN
  qq
   ð
  ö
  A2747765 508 bp DNA linear GSS 25-JAN-2001
RPCI-24-99M13.TJ RPCI-24 Mus musculus genomic clone RPCI-24-99M13,
DNA sequence.
   ö
   Zhao,S., Nierman,W., Malek,J., Shatsman,S., Akinret,B., Levins,M., Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A., Gebregeorgis,E., Russell,D., de Jong.P. and Fraser,C.M.
Mouse BAC End Sequences from Library RPCI-24
Unpublished (1999)
Other_GSSs: RPCI-4-99M13.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
7712 Medical Center Dr., Rockville, MD 20850, USA
TTel: 301 838 0200
Fax: 301 838 0200
   Email: szlacétyr.org
Clones are derived from the mouse BAC library RPCI-24. For BAC
Clones are derived from the mouse BAC library availability, please contact Pieter de Jong
(pdeJong@mail.cho.org). Clones may be purchased from BACPAC
Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 99 row. M column: 13
Seq primer: SP6
Class: BAC ends.
  /strain="C57BL/6J"
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/sex="Male"
/sex="Male"
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/note="Vector: pTARBACI; Site_1: BamH1; Site_2: BamH1;
/note="Vector: pTARBACI; Site_1: BamH1; Site_5: BamH1;
/note="Vector: pTARBACI; Site_5: BamH1; Site
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
1 (bases 1 to 508)
   Gaps
   Gaps
   ö
   ő
   Length 508;
   Length 496;
  Indels
  Indels
  Score 19; DB 9; Le
Pred. No. 1.5e+02;
Mismatches 0;
   1.8%; Score 19; DB 12; L
100.0%; Pred. No. 1.5e+02;
iive 0; Mismatches 0;
Soares and M.Fatima Bonaldo."
   154 t
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1. .508
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  Query Match
1.8%; Score 19;
Best Local Similarity 100.0%; Pred. No.
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  97 9
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  422 CCCTGGTCATCCTGGGAAC 440
   287 CCTGGTCATCCTGGGAAC 269
   907 GGACACTCAAAAACACAAA 925
   232 GGACACTCAAAAACACAAA 250
                        106 c
   89
C
   Conservative
  Mus musculus
  house mouse.
  Best Local Similarity
Matches 19; Conserv
                        117 а
   Query Match
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                        BASE COUNT
ORIGIN
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  ORGANISM
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JOURNAL
COMMENT
   BASE COUNT
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AZ747765
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  VERSION
KEYWORDS
SOURCE
  REFERENCE
   AUTHORS
   FEATURES
  ORIGIN
```

ö

Gaps

g ð

```
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                         Tel: 314 286 1800
Fax: 314 286 1810
  Best Local Similarity
   Homo sapiens
   human.
  19;
   Query Match
  source
  source
   RESULT 40
AQ535999/c
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   ACCESSION
   VERSION
KEYWORDS
SOURCE
   REFERENCE
  AUTHORS
   JOURNAL
  FEATURES
  FEATURES
   TITLE
   COMMENT
  ORIGIN
  ð
   ద
   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 518)

Hiller, L. Lennon, G., Becker, M., Bonaldo, M. F., Chiapelli, B., Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Legy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M. B., Tan, F., Thierry-Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M. Generation and analysis of 280,000 human expressed sequence tags
  /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
Cool: Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
ECORI sites. The ligation products were transformed into
BH10B electrocompetent cells (BRE Life Technologies).

126 c 100 g 138 t
   EST 31-DEC-1996
  ö
  Email: szhaofetjer.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://wacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/Dac_ends/mouse/bac_end_intro.html
Levins, M., Mcgann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P.
   AA180359 519 518 bp mRNA linear EST 31-DEC-199 zp15g07.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone mAAE:609564 3', mRNA sequence.
   Gaps
  ö
   Length 515;
                                Whose BAC End Sequences from Library RPCI-23 Unpublished (1999)
Other_GSSs: RPCI-23-42F8.TJ
Contact: Shaying Labo
Department of Eukaryotic Genomics
The Institute for Genomic Research
712 Medical Center Dr., Rockville, MD 20850, USA
712: 301 838 0200
  0; Indels
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  Contact: Wilson RK
Washington University School of Medicine
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1. 515
7. 7019018m="Mus musculus"
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ORIGIN
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JOURNAL
COMMENT
  JOURNAL
MEDLINE
  ACCESSION
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  AUTHORS
  AA180359
  FEATURES
  COMMENT
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Uppublished (1997)
Other_GSSS: RPCT-11-318M7.TV
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 3
Email: estGwatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
IMAGE consortum (info@image.llnl.gov) for further information.
Seq primer: -40ML3 kd. from Amersham
High quality sequence stop: 382.
Location/Qualifiers

1. 518
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   AQ335999 518 bp DNA linear GSS 18-MAY-1999
RPCI-11-318M7.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-318M7,
DNA sequence.
   ö
   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 518)
   Zhao, S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and Venter
   Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready Map Building
   Gaps
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  0; Indels
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Double-strain cDNA synthesized with the mRNA isolated from adult worm, was inserted into the bacteriophage from adult worm, was inserted into the bacteriophage lambda gill Sfi-Not arms between EcoRI and NotI site of the Lacz gene. The CDNA library was contructed by Chen S. Z. at Nanjing Medical University, Nanjing, Jiangsu, P.R. China. (See: Chen Shuzhen, et al. Chinese Journal of Zonoses 1997,13(6): 23-25)"
  LOCUS B1677745 SEP-2001 DEFINITION CLS447 CLS (Cambium and bark region of black locust - Summer)
   EST 10-DEC-1999
  Department of Parasitology
Sun-Yat-sen University of Medical Sciences
Sun-Yat-sen University of Medical Sciences
Sun-Yat-sen University of Medical Sciences
Tel: 86-20-87330566
Fax: 86-20-87331679
Email: zdwu62@163.net
  JAYL0146.GYL Schistosoma japonicum Lambda gtll Express library Schistosoma japonicum cDNA clone JAYL0146.GY 5', mRNA sequence.
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  1 (bases I to 554)
Li,Y., Wu,Z.D. and Yu,X.B.
Expressed sequence tags from adults of Schistosoma japonicum (Chinese strain) (Li,Y.; Wu,Z.D.; Yu,X.B.)
Contact: Wu ZD
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Live 0; Mismatches 0;
   mRNA
   FORWARD: Lambda gtll Forward Primer BACKWARD: Lambda gtll Reverse Primer Seq primer: Lambda gtll Forward Primer High quality sequence stop: 554.
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100.08; Pr
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  Schistosoma japonicum.
Schistosoma japonicum
   308 CCTGCCCAGCGTGTCTGCT 290
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   566 TCGCCATCATCTATTTG 584
  375 TCGGCATCATCTTATTTG 393
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Matches 19; Conservative
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  ACCESSION
  VERSION
KEYWORDS
   RESULT 42
   REFERENCE
  JOURNAL
   AW231247
LOCUS
   FEATURES
  COMMENT
  ORIGIN
   ò
  δ
  q
  d
d
  Shao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akinret, B., Levins, M., Mcgann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P. and Frasar, C.M.

Mouse BAC End Sequences from Library RPCI-23

Unpublished (1999)

Other_GSSS: RPCI-23-73N16.TV

Contact: Shaying Zhao

Contact: Shaying Zhao

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0200

Fax: 301 838 0200

Email: szhaodetigr.org

Clones are derived from the mouse BAC library RPCI-23. For BAC

library availability, please contact Pieter de Jong

(pleterGeloiqu.med buffalo.edu). Clones may be purchased from

BACPAC Resources (http://wpcac.med.buffalo.edu/orderingframe.htm)

or from Resea ch Genetics (Info@resgen.com). BAC end page:

http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html

Plate: 73 row: N column: 16

Seq primer: Sp6

Class: BAC ends
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brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACc3.6 vector at the
ECORI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies).

135 c 112 g 144 t
  S45 bp DNA linear GSS 15-JUN-2000 RPCI-23-73N16.TJ RPCI-23 Mus musculus genomic clone RPCI-23-73N16, AZ239913
   ö
   house mouse.

Mus musculus

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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   DB 12; Length 545;
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0; Mismatches 0;
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Best Local Similarity 100.0%; Pr
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  189 CCTTATGATCTGCCTGCCT 207
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A2239913/c
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DEFINITION
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ORGANISM
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ORIGIN
   BASE COUNT
ORIGIN
   TITLE
JOURNAL
COMMENT
  ACCESSION
  VERSION
KEYWORDS
  REFERENCE
  AUTHORS
   FEATURES
  셤
  ò
```

```
Mus musculus
   Best Local Similarity
Matches 19; Conserv
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  DEFINITION
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  AQ993291/c
  ORGANISM
  TITLE
JOURNAL
  Matches
   ACCESSION
  VERSION
KEYWORDS
SOURCE
   REFERENCE
   AUTHORS
   FEATURES
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   COMMENT
   RESULT
   ORIGIN
  ò
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bass 1 to 577)
1 (bass 1 to 577)
1 (bass 1 to 577)
2 Zhao, S., Nerman, W., Feldblyum, T., Malek, J., Shatsman, S., Akinret, B., Levins, M., Mcgann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P., and Fraser, C.M.
Mouse BAC End Sequences from Library RPCI-23
1 Unpublished (1999)
2 Conter_GSS: RPCI-23-286k10.TV
Conter_GSS: RPCI-23-286k10.TV
Conter_CSS: RPCI-23-286k10.TV
Conter_Libraryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
   577 bp DNA linear GSS 01-MAR-2000
, DNA sequence.
A2041597.1 GI:7134231
GSS.
   Crismary / Listance | Cambian region (Cambium and bark region of black locust - Summer)" / dev.stage="mature tree" / fev.stage="mature tree" / note="Vector: lambda TriplEx; Site_1: Sfi IA; Site_2: Sfi IB; The CDNA library was made from the cambium and bark region of a mature black locust tree collected in Michigan
  ö
   Robinia pseudoacacia
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papillonoideae; Robinieae;
   /db_xref-"taxon:35998"
/clone_11b-"CLS (Cambium and bark region of black locust
  1 (bases 1 to 556)
Han, K.-H., Yang, J., Park, S., Paule, C.R., Kapur, V., Retzel, E.F., Kamdem, D.P. and Keathley, D.E.
Analysis of gene expression patterns in trunk wood of a mature black locust (Robinia pseudoacacia)
  Gaps
  ö
  Michigan State University
126 Natural Resources, East Lansing, MI 48824-1222, USA
Tel: 517 353 4751
Fax: 517 432 1143
Email: hanky@msu.edu.
  Length 556;
  Indels
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1.8%; Score 19; DB 10; 1
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 19; Conservative 0; Mismatches 0;
Robinia pseudoacacia cDNA, mRNA sequence.
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  Location/Qualifiers
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  134 9
   Contact: Kyung-Hwan Han
Department of Forestry
                                      BI677745.1 GI:15630652
   in late July.
  244 GCTTTTGGGGACATTCCCT 262
  169 GCTTTTGGGGACATTCCCT 151
  Robinia pseudoacacia.
  Mus musculus
   house mouse.
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VERSION
KEYWORDS
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ORGANISM
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JOURNAL
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  REFERENCE
   AUTHORS
  JOURNAL
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KEYWORDS
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   AUTHORS
  FEATURES
   TITLE
   COMMENT
  ò
   g
```

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CooR: Site_2: EcoR: Female C57BL65 mouses kidney and/or
brain genomic DNA was isolated and partially digested
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selected DNA was cloned into the pBACe3.6 vector at the
ECORI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies).
   FPCI-23-331E8.TVB RPCI-23 Mus musculus genomic clone RPCI-23-331E8, AQ993291
   Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S., Akinret,B., Levins,M., Mogann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P. and Fraser,C.M.
Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Fex: 301 838 0200
  ö
Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
library availability, please contact Pieter de Jong
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 286 row: K column: 10
   Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 594)
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  ö
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source

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  ö
  Gaps
  ö
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  Search completed: October 29, 2002, 04:51:15 Job time : 1756 secs
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ORIGIN
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GenCore version 5.1.3

Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 29, 2002, 02:40:58; Search time 1723 Seconds

(without alignments)

8154.574 Million cell updates/sec

1041

Sequence: US-09-886-041-1

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Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000
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2: em\_esthum:\*
4: em\_esthum:\*
5: em\_estov:\*
6: em\_estpl:\*
7: em\_estpl:\*
10: gb\_est1:\*
10: gb\_est1:\*
11: gb\_hcs:\*
12: gb\_gs:\*
13: em\_gss\_hum:\*
14: em\_gss\_lnv:\*
16: em\_gss\_lnv:\*
16: em\_gss\_lnv:\*
16: em\_gss\_lnv:\*

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

EST:\*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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| SUMMARIES | QI                            | AF345568           | AL545172          | AL546894          | BI837965           | AL554198          | BI820995           | BI908162           | BM008116           | BB873518          | BB614132          | BB873597          | BB849390          | BF074336           | BI489649           | BF230383           | BI521556           | вв866696          |  |
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|           | %<br>Query<br>Match Length DB | 1372               | 870               | 882               | 801                | 855               | 876                | 734                | 752                | 367               | 099               | 367               | 422               | 550                | 636                | 532                | 938                | 209               |  |
|           | %<br>Query<br>Match           | 100.0              | 30.5              | 30.5              | 29.7               | 27.8              | 26.8               | 26.0               | 25.7               | 24.6              | 24.5              | 24.3              | 22.1              | 21.0               | 20.7               | 20.5               | 20.0               | 18.9              |  |
|           | Score                         | 1041               | 317.2             | 317.2             | 309                | 289.4             | 278.6              | 270.4              | 267.2              | 255.8             | 254.6             | 253.2             | 230               | 218.2              | 215.8              | 213.8              | 208.6              | 196.6             |  |
|           | Result<br>No.                 | -                  | 7                 | ٣                 | ₹                  | S                 | 9                  | 7                  | æ                  | σ                 | 10                | 11                | 12                | 13                 | 14                 | 15                 | 16                 | 17                |  |

| 18 195.4 18.8 689 9 BB61309 20 178 13 17.6 619 10 BI561009 21 176 8 17.0 638 9 BB61057 22 169.4 16.3 647 9 10 BI522957 22 156.4 16.3 16.1 0166 12 AGI1497 22 166.8 16.0 1016 12 AGI1497 22 122.5 11.8 10.7 69 9 BB656095 29 118 11.3 649 9 BB656095 29 122.5 11.8 10.7 69 9 BB656095 29 118 11.3 649 12 AZ28727 27 122.5 11.8 10.7 10 BI5611829 29 118 11.3 649 12 AZ28725 21 10.5 10.1 805 10 BB71829 31 10.0 9 9 10 BI71829 32 10.5 9 9 99 12 CNSOSER 33 10.0 9 9 1856095 41 84.2 8.1 694 10 BI541931 38 85.8 8.2 609 10 BI51191 38 87.8 8.2 609 9 ALS888 100.0 9 5.2 8.2 609 9 ALS889 44 84.2 8.1 663 10 BI542996 45 84.2 8.1 663 10 BF74596 46 84.2 8.1 663 10 BF74596 47 84.2 8.1 693 10 BF74596 48.2 8.1 693 10 BF74596 48.4 84.5 88 AF74568  CAS. ACCESSION AF74568 ACCESSION AF74674 ACCESSION AF74676 ACC | BB613494 BB613494 B1961009 MONOL_S_A B1961009 MONOL_S_A B1961057 BB661057 BB645691 BB645691 AL346581 TEATRACOICA AR346581 TEATRACOICA AR361289 Pan troogl AR346581 TEATRACOICA AR361289 Pan troogl AR361289 CM3-HF080 B190118 60305522 BB636095 BB636095 BB712299 CM3-HF080 BG74555 RPCI-23-4 AL210941 TEATRACOICA BA42651 BP636095 BC013202 HOMO SBP1 AL211932 TEATRACOICA BA42651 BB636095 BF9074 MONOL_3_D B1961697 MONOL_3_D | NTS        | mRNA linear HTC 13-JUL-2001<br>receptor (FKSG80) mRNA, complete |                          | Craniata; Vertebrata; Euteleostomi;<br>Catarrhini; Hominidae; Homo. | a novel gene encoding a putative |                             | FENGKESHENG F              | Chang Street, Xuanwu        | E 00               |      | 1421182 /gene="FKSG80" /gene="FKSG80" /codon_start=1 /product="putative chemokine receptor" /product="putative chemokine receptor" /product="putative" /product="putative" /product="putative" /product="putative" /db_xref="GI.13519964" /dccaptor="GI.13519964" /dccaptor="GI.135199999999999999999999999999999999999 |
|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------|-----------------------------------------------------------------|--------------------------|---------------------------------------------------------------------|----------------------------------|-----------------------------|----------------------------|-----------------------------|--------------------|------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------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| AF345568  AF34568  AF34 |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |            | tive                                                            | 5179                     | a; C                                                                | ng, L                            | 72)                         | -200                       | 4 To<br>'R'.                | E E                |      | KSG8<br>KSG8<br>KSG8<br>Itart<br>id<br>id<br>id<br>id<br>id<br>id<br>id<br>id<br>id<br>id<br>id<br>id<br>id                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
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                                       | g, Yg.                           | mokine<br>ublishe<br>(bases | g,Yg.<br>ect Sub<br>mitted | hnology<br>jing 10          | H / / /            | \n \ | /u / / / / X H F                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| υν Γροσωνίζι ο ο ο ο απαπαπαπαπα                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       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                                                                                                                                                                                                                                                                       |            | AF3<br>Hom                                                      | AF3<br>AF3<br>AF3<br>HTC | HOH<br>Euk<br>Man                                                   | Wan<br>Mol                       | on b                        | wan<br>Dir<br>Sub          | Tec                         |                    |      |                                                                                                                                                                                                                                                                                                                                                                                                                         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                                                                                                                                                                                                                                                                       |            | RES<br>AF3<br>LOC<br>DEF                                        | ACC<br>VER<br>KEY<br>SOU | 0 6                                                                 | 4 F                              | JREF                        | 4 H D                      | FEA                         |                    |      |                                                                                                                                                                                                                                                                                                                                                                                                                         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Life Technologies. Contact : Feng Liang Life Technologies.
a division of Invitrogen 9800 Medical Center Drive
Exceville, Maryland 20850, USA Fex: (1) 301 610 8371
Email : filangelifetech.com URL :
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Email: cgapbs-rémail.nih.gov
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Life Technologies, Inc.
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CDNA Library Preparation: Life Technologies, Inc.
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   AUTHORS
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   | 1. .734 | Arganism=Homo sapiens | Arganism=Homo sapi
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   Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: capaber: Fimilinih.gov
Email: capaber: Fimilinih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
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Tissue Procurement: Dr. Mark Watson
Tissue Procurement: Dr. Mark Watson
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CDNA Library Preparation: Ling Hong/Rubin Laboratory
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
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**Atimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K., Ishii, Y., Tto, M., Kawal, J., Kojina, Y., Kondo, M., Matsuyama, T., Makamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takaku-Akhaira, S., Tanaka, T., Tomaru, A., Towaruki, A., Takaulshika, Muramatsu, M. and Hayashizaki, Y. RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al.
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   Unpublished (2001)

Contact: Yoshihide Hayashizaki

Laboratorry for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
The Institute of Physical and Chemical Research (TREN)
Tel: 81-45-503-922
Tel: 81-45-503-9216
   Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci.P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
M., Konnoh., Okazaki,Y., Muramatsus,M. and Hayashzaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
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Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Roya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki
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Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K., Ishii, Y., Tto, M., Kawal, J., Koliam, M., Matsuyama, T., Y., Tto, M., Kawal, J., Koliam, Y., Kondo, M., Matsuyama, T., Salto, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanakaya, T., Tomaru, A., Towarisi, M., Watahiki, A., Yasanishi, A., Muramatsu, M. and Hayashizaki, Y. RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al.
   Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
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  RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. .10 (11), 1757-1771 (2000) (
  encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
'D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.

RIKEN Mouse ESTS (Arakawa,T., et al. 2001)
Unpublished (2001)
Contact: Yoshinide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC). Yokohama Institute
1-722 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-922
   Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
'M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapped discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
waci,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
watahiki,M., Yoneda,Y., Ishikwwa,T., Ozawa,K., Tanaka,T., Matsuura
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  3/j. CDNA was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."
   Hayashizaki,Y. Computational Analysis of Full-Length Mouse CDNAs Compared with
   Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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   Email: genome-resegac.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninci.P., Shibata.K., Hayatsu.M., and Hayashizaki.Y.
M., Konno,H., Okazaki.Y., Muramatsu.M. and Hayashizaki.Y.
Normalization and subtraction of cap-trapper-selected connas to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi.K., Fujiwake,S., Inoue,K., Togawa,K., Tawaka,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1557-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.
  ö
  EST 26-NOV-2001
                    The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
18-1: 81-45-503-9216
Fax: 81-45-503-9216
   BB849390 RIKEN full-length enriched, adult inner ear Mus musculus
  Computer based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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  121 TGCTTCCACATGAAGACCTGGAAGCCCAGCACTGTTTACCTTTTCAATTTGGCCGTGGCT 180
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DEFINITION
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   82
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  322
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Unpublished (2001)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suchiro-Cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9216
Fax:   RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 110 (11), 1757-1771 (2000) Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara
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Matches 330; Conservative (
   Y. and Hayashizaki, Y
  house mouse.
BB84939(
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492 301 552

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636 bp mRNA linear EST 28-AUG-2001
NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5173205 5',
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Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 11 to 636)

11 (bases 12 to 636)

12 (bases 11 to 636)

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
  315
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   Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone disfribution: MGC clone distribution information can k
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: Librariatal row: d column: 06
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1 (bases I to 550)

2 (bases I to 550)

3 (bases I.c., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keele, J.W.
   Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
USDA, ARS, US Meat Animal Research Center
USDA, ARS, US Meat Animal Research Center,
Tel: 402 762 436
Fax: 402 762 4390
Fax: 403 762 430
Fax: 403 762 43
   EST 25-APR-2001
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   libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
21180013
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

MEDLINE COMMENT

JOURNAL

TITLE

BASE COUNT

FEATURES

RESULT 13 BF074336 LOCUS DEFINITION

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ORIGIN
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   196
   256
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oligo-dT primed and directionally cloned (EcoRv site is
estroyed upon cloning). Average insert size 18 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: tis sis a NIL MC Library."
   Wells, K.D.
Mapping of Expressed Sequence Tags from a normalized bovine mammary gland cDNA library
Unpublished (2000)
Contact: Sonstegard TS
  ö
   EST 14-NOV-2000
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Sonstegard,T.S., Capuco,A.V., Van Tassell,C.P., Ashwell,M.S.
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BF230383
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   JOURNAL
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  AUTHORS
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Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and 'minmatch 12 options.
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  ö
USDA, ARS, Beltsville Agricultural Research Center Bdlg. 200 Rm 2A, Beltsville, MD 20705, USA Pel: 301 504 8416 Fax: 301 504 8414 Email: tads@lpsi.barc.usda.gov
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Run on:

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Result

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ORGANISM: Rat ORGANISM: Rat PUBLICATION INFORMATION: AUTHORS: Hadcock Dr., John R. AUTHORS: Dr. Ozenberger, Bradley A. AUTHORS: Dr. Pausch, Mark H. TILLE: Receptor Identification Method DATE: 17-JUL-1992

ANTI-SENSE: NO ORIGINAL SOURCE

Sequence 7 Sequence 7 Sequence 1 Sequence 1

100 922.5 922.6 922.6 811.7 788.2 778.2 778.2 775.8 775.8

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US-08-472-840-3 US-08-476-976-3

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US-08-853-194-1
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Patent No. 5929209
GENERAL INFORMATION:
APPLICANT: Ozenberger Dr., Bradley A.
APPLICANT: Pausch Dr., Mark H.
TITLE OF INVENTION: Receptor Identification Method
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ANDRESS:
ADDRESSEE: American Home Products Corporation
  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/771,182 FILING DATE: 20-DEC-1996 CLASSIFICATION: 435
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Pred. No. 4.5e-57;
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COUNTRY: USA
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Pred. No. 4.5e-57;
0; Mismatches 189;
  AUTHORS: Dr. Ozenberger, Bradley A. AUTHORS: Dr. Pausch, Mark H. TITLE: Receptor Identification Method DATE: 20-DEC-1996
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TELERAX: 201-683-4117
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AUTHORS: Dr. Ozenberger, Brad
                      32,269
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Matches 356; Conservative
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PUBLICATION INFORMATION:
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APPLICANT: MOONEY, DEFREY
APPLICANT: BERGSHA, DERK
APPLICANT: HALSEY, WENDY
TITLE OF INVENTION: CDNA CLONE HEOAD54 THAT ENCODES
CORRESPONDENCES: 4
CORRESPONDENCE ADDRESS:
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SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/955,713
FILING DATE: 23-0CT-1997
CLASSIFICATION 1-435
PRIOR APPLICATION NATA:
APPLICATION NUMBER: 60/050,124
FILING DATE: 18-JUN-1997
ATTORNEY, AGENT INFORMATION:
NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,031
   REFERENCE/DOCKET NUMBER: GH-70087
TELECOMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0701
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Patent.No. 5955308
GENERAL INFORMATION:
  SSEE: RATNER & PRESTIA
I: P.O. BOX 980
VALLEY FORGE
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US-08-955-713-1
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APPLICANT: Hadcock Dr., John R.
APPLICANT: Ozenberger Dr., Bradley A.
APPLICANT: PRUSCH Dr., Mark H.
TITLE OF INVENTION: Receptor Identification Method
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
  COUPTER: United States of America
ZIP: 06904-0060
ZIP: 06904-0060
COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/853,194
  Query Match 22.1%; Score 229.6; DB 3; Best Local Similarity 65.0%; Pred. No. 4.5e-57; Matches 356; Conservative 0; Mismatches 189;
   HUTHORS: Hadcock Dr., John R.
HUTHORS: Dr. Ozenberger, Bradley A.
HUTHORS: Dr. Pausch, Mark
TILE: Receptor Identification Method
DATE: 17-JUL-1992
   STREET: One Cyanamid Company STREET: One Cyanamid Plaza CITY: Wayne
   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/915,966
FILING DATE: 17-JUL-1992
ATTORNEY/AGENT INFORMATION:
  31829-00
  NAME: Tsevdos Dr., Estelle J. REGISTRATION NUMBER: 31,145
REFERENCE/POCKET NUMBER: 31829
TELECOMMUNICATION INFORMATION:
TELEPHONE: 203-321-2361
TELEFAX: 203-321-2971
Sequence 1, Application US/08853194
Patent No. 6077666
   TELEPHONE.
TELERAX: 203-321-2.
TELERX: 710-474-4059
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 545 base pairs
"VPE: nucleic acid
   ORGANISM: Rat
PUBLICATION INFORMATION:
  MOLECULE TYPE: CDNA HYPOTHETICAL: NO ANT.-
  ANTI-SENSE: NO ORIGINAL SOURCE:
   FILING DATE:
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53 TGCCGCCGCTGCTCATTGTGGCCTTTGTGCTGGGCGCACTAGGCAATGGGGTCGCCTGT 112
   113 GTGGTTTCTGCTTCCACATGAAGACCTGGAAGCCCAGCACTGTTTACCTTTTCAATTTGG 172
  138 rescente actractication and action action and action 
  233 GTAGACACTGGGCTTTTGGGGACATTCCCTGCCGAGTGGGGGCTCTTCACGTTGGCCATGA 292
  318 TGCANCCCCACCACGTGCTGAACCGTGCTTCCGTGGGGGCANCTGCCCGGGTGGNCGGGG 377
   378 GAATCIGGG -- - TGGGCATCCTGCTCCTCAACGGGNACCTGCTCCTGAACACCTTCTCCG 434
   533 ACATCATGTTCCAGCTGGAGTTCTTTATGCCCCTCGGCATCATCTTATTTTGCTCCTTCA 592
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   198 ATGAGACCTGGCGCTTTGGGGCTGCTGCCTGCAAAGTCAACCTCTTCATGCTGTCNACCA
   173 CCGTGGCTGATTTCCTCCTTATGATCTGCCTGCCTTTTCGGACAGACTATTACCTCAGAC
   353 TCCACCCCCACCACGCGGTGAACACTATCTCCACCGGGTGGCGGGCTGGCATCGTCTGCA
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  18.1%; Score 188; DB 2; Length 1435; Ilarity 54.1%; Pred. No. 7.9e-45; Conservative 3; Mismatches 359; Indels 1:
  OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/955,713
FILING DATE: 23-6CT-1997
CLASSIFICATION: 435
   GH-70087
   APPLICATION NUMBER: 60/050,124
FILING DATE: 18-JUN-1997
ATTORNEY/AGENT INFORMATION:
AMBE: PRESTIA, PAUL F
REJSTRATION NUMBER: 23,031
          ADDRESSEE: RATNER & PRESTIA STREET: P.O. BOX 980
   REFERENCE DOCKET NUMBER: GH
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
  TELEX: 846L69
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1435 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
   IBM Compatible
  Diskette
  610-407-0701
   PRIOR APPLICATION DATA:
   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                      STREET: P.O. BOX 9 CITY: VALLEY FORGE
  COMPUTER: IBM CON OPERATING SYSTEM:
   linear
  Similarity
   USA
   MOLECULE TYPE:
  TOPOLOGY:
  TELEFAX:
  Matches 440;
   COUNTRY:
   US-08-955-713-3
  STATE:
   Query Match
  Best Local
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   1173 TCTTTGGCATGCCTTCCATGGTGGTTTCTGGCTGTCCGCCTGCCGCTCCCTGGACCTCT 1232
   412
   ACATCATGTTCCAGGTGGAGTTCTTATGCCCCTCGGCATCATCTTATTTTGCTCCTTCA 592
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       Length 1594;
   Sequence 3, Application US/08955713
Patent No. 5955308
GENERAL INFORMATION:
APPLICANT: ASTHE, GANESH
APPLICANT: MOONEY, JEFFREY
APPLICANT: BERGSMA, DERK
APPLICANT: BALSEY, WENDY
TITLE OF INVENTION: CDNA CLONE HEOAD54 THAT ENCODES
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
   Score 188.8; DB 2;
Pred. No. 4.9e-45;
); Mismatches 357;
  827 TGGTGTATTTTTCAAGCCCCTCCTTTCCCAA 860
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Similarity 54.7%;
5; Conservative (
  445;
   SULT 5
-08-955-713-3
       Query Match
  Matches
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  779 regerrearacercesarereacesceaecreaecracerscacacacrererereaeces 838
   421
  359 GGCTTAAGGTCAACCTGCTGTGTCTCTCAGGCGGCCCTGGGGGTCTCGGGCTCTGGC
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   422 CCCTGGTCATCCTGGGAACAGTGTATCTTTGCTGGAGAACCATCTCTGCGTGCAAGAGA
  419 recrearegreereacereaceregeerreerearerereagecegeeeraaacreea
   479 CCAGGTGCCACAGTTTCTACTCCAGGGCAGACGGCTCCTTCAGCATCATCTGGCAGGAAG
   536 TCATGTTCCAGCTGGAGTTCTTTATGCCCCTCGGCATCATCTTATTTTGCTCCTTCAAGA
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  713 CTGCTAGACT-CTATTTCCTCTGGACGGTGCCCTCGAGTGCCTGCGATCCCTCTGTCCAT
   GGGGCCCT - - - - GCACATAACCCTCAGCTTCACCTACATGAACAGCATGCTGGATCCCC
   59 recrescenceastrassersestrassersestrassersessestrasserses of recrescent of the contract of t
  182 ATTTCCTCCTTATGATCTGCCTGCCTTTTCGGACAGACTATTACCTCAGACGTAGACACT
  179 ACCTGCTGTTGGCTGCGTGCCTTTTCCTGGCCGCCTTCTTACCTGAGCCTCCAGGCTT
   242 GGGCTTTTGGGGACATTCCCTGCCGAGTGGGGCTCTTCACGTTGGCCATGAACAGGGCCG
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  653 CGACCCGGTTCATCATGGTGGTGGCAATTGTGTTTCATCACATGCTACCTGCCCAGCGTGT
  122 GCTTCCACATGAAGACCTGGAAGCCCAGCACTGTTTACCTTTTCAATTTGGCCGTGGCTG
   302 GGAGCATCGTGTTCCTTACGGTGGTGGCTGCGGACAGGTATTTCAAAGTGGTCCACCCC
  827 TGGTGTATTATTTTCAAGCCCCTCCTTTCCCAAATTCTACAACAAGCTC 876
  Sequence 1, Application US/09130749; Patent No. 6031344; Patent No. 6031344; SEMERAL INFORMATION: STABON, USMAN APPLICANT: SLABON, USMAN APPLICANT: ELSHOURBAGY, NABIL TITLE OF INVENTION: RECEPTOR (GPR31A); PITLE OF INVENTION: RECEPTOR (GPR31A); NUMBER OF SEQUENCES: 2 CORRESPONDENCE ADDRESS: ADDRESSEE: RATNER & PRESTIA; STREET: P.O. BOX 980; CITY: Valley Forge STATE: PA
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   CGACCCGGTTCATCATGGTGGTGCAATTGTGTTCATCACATGCTACCTGCCCAGCGTGT 712
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  Gaps
  713 CTGCTAGACTCTATTTCCTCTGGACGGTGCCCTCGAGTGCCTGGGATCCCTCTGTCCATG
   593 AGATTGTTTGGAGCCTGAGGCGGAGGCAGCTGGCCAGACAGGCTCGGATGAAGAGG
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  15;
   Length 960;
   Indels
   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRINT APPLICATION DATA:
FILING DATE: 07-Aug-1998
CLASSIFICATION: UNKNOWN
   A 7TM
  Query Match 13.4%; Score 139.2; DB 3; Best Local Similarity 51.4%; Pred. No. 8.6e-31; Matches 427; Conservative 0; Mismatches 388;
   PRIOR APPLICATION DATA:

APPLICATION NUMBER: <UNKNOWN>
FILING DATE: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:

NAME: PRESTIA, PAUL F.

REGISTRATION NUMBER: 23,031

RELECOMMUNICATION INFORMATION:

TELECHONE: 610-407-0700
   ELSHOURBAGY, NABIL TITLE OF INVENTION: MOLECULAR CLONING OF
  827 TGGTGTATTTTTCAAGCCCCTCCTTTCCCAA 860
   792 TGCTCTACTGCTTCTAGCCCCAACTTCCTCCA 825
   RECEPTOR (GPR31A)
   ) MOLECULE TYPE: CDNA
) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-130-749-1
   CORRESPONDENCE ADDRESS:
ADDRESSEE: RATWER & PRESTIA
STREET: P.O. Box 980
CITY: Valley Forge
  Sequence 1, Application US/09130749
Patent No. 6031090
GENERAL INFORMATION:
APPLICANT: SHABON, USMAN
  LENGTH: 960 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
  TELEFAX: 610-407-0701
  TELEX: 846169
INFORMATION FOR SEQ ID NO: 1:
   SEQUENCE CHARACTERISTICS
  TOPOLOGY: linear
   NUMBER OF SEQUENCES:
   USA
   STATE: PA
   ZIP: 19482
  COUNTRY:
  RESULT 6
US-09-130-749-1
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599 TCATCAGGGCTCTCCAGAAAAGACTCCGGGAGCCTGAGAAACAGCCCCAAGCTTCAGCGGG 658
  713 CTGCTAGACT-CTATTTCCTCTGGACGGTGCCCTCGAGTGCCTGCGATCCCTCTGTCCAT 771
  719 TGGCCAGAGTCCTGATGCACATCTTCCAGAATCTGGGGAGCTGCAGGGCCCTTTGTGCAG 778
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  Sequence 43, Application US/08153848
Sequence 43, Application US/08153848
Sequence 43, Application US/08153848
Sequence 43, Application US/08153848
Sequence 43, Application:
APPLICANT: Godalska, Ronald
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: No. 5759804el Seven Transmembrane Receptors NUMBER OF SEQUENCES: 64
CORRESPONDENCES: 64
CORRESPONDENCE ADDRESS: ADDRESSE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Bicknell
   6
   10.5%; Score 109; DB 1; Length 1901; 47.1%; Pred. No. 6.6e-22; tive 0; Mismatches 415; Indels
  827 IGGIGIATTATTTTCAAGCCCCTCCTTTCCCAAATTCTACAACAAGCTC 876
  6300 Sears Tower, 233 South Wacker Drive
   ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA #1.00
   CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5759804and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
TELECHONE: (312) 474-6300
TELEFAX: (312) 474-6408
TELEFAX: 25-3856
INFORMATION FOR SEO ID NO: 43:
SEQUENCE CHARACTERISTICS:
   APPLICATION NUMBER: US/08/153,848
   DNA (genomic)
   LENGTH: 1901 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
  Query Match 10.58
Best Local Similarity 47.18
Matches 377; Conservative
   CDS
701..1717
   CITY: Chicago
STATE: Illinois
   MOLECULE TYPE:
   ; NAME/KEY:
; LOCATION:
US-08-153-848-43
   TOPOLOGY:
   RESULT 8
US-08-153-848-43
  COUNTRY:
  STREET:
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  119 TGTTCCGGGTCAGGGTGTGGGAAGCCGTACGTGTCTACCTGCTCAACCTGGCCTGGCTG 178
   182 ATTTCCTCCTTATGATCTGCCTGCCTTTTCGGACAGACTATTACCTCAGACGTAGACACT 241
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  419 TCCTGATGGTCGCCCTCACCTGCCCGGGCTTGCTCATCTCTGAGGCCGCCCCAGAACTCCA 478
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   299 TGGGGATGGCCTTCCTGGCCGCGGGGCTTTGGACCGGTACCTCCGTGTGGTCCACCTC 358
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Pred. No. 8.6e-31;
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   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/09/130,749
FILING DATE: 07-AUG-1998
CLASSIFICATION:
PRIOR APPLICATION NUMBER:
FILING DATE:
FILING DATE:
   REFERENCE/DOCKET NUMBER: GP-70513
TELECOMUNISCATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0701
  ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,031
  Query Match 13.4%;
Best Local Similarity 51.4%;
Matches 427; Conservative
  TELEX: 846169
INFORMATION FOR EXQ. ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 960 base palrs
TYPE: nucleic acid
STRANDENESS: single
TOPOLOGY: linear
  MOLECULE TYPE: CDNA
  Query Match
Best Local Similarity
   US-09-130-749-1
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Query Match
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   1036 CCTCAACATGTACGCCAGCATCTACTTCCTCACCTGCATCAGCGCCGACCGTTTCCTGGC 1095
   1216 CGTGCAGACCAACCACACGGTGGTCTGCCTGCAGCTGTACCGGGAGAAGGCCTCCCACCA 1275
   276 IGCCCIGGIGCCCIGGCAGIGGCCTICACCTICCCGTICATCACCACGGICACCTGCTA 1335
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  648 GAAGGCGACCCGGTTCATCGTGGTGGCAATTGT-----GTTCATCACATGCTA 698
  699 CCTGCCCAGCGTGTCTGCTAGACTCTATTTCCTCTGGACGGTGCCCTCGAGTGCCTGCGA 758
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   CAGACGTAGACACTGGGGCTTTTGGGGACATTCCCTGCCGAGTGGGGGCTCTTCACGTTGGC 287
  108 CCTGTGTGTTTCTGCTTCCACATGAAGACCTGGAAGCCCAGCACTGTTTACCTTTTCAA 167
  168 TITGGCCGTGGCTGATITCCTCCTTATGATCTGCCTGCCTTTTCGGACAGACTATTACCT 227
48 GGTGATGCCGCCGCTGCTCATTGTGGCCTTTGTGCTGGGCGCACTAGGCAATGGGGTCGC 107
                288 CATGAACAGGGCCGGGAGCATCGTGTTCCTTACGGTGGTGGTGCTGCGGACAGGTATTTCAA
   468 CIGCGTGCAAGAGACGGCCGTCICCTGTGAGAGCTTCATCATGGAGTCGGCCAATGGCTG
  588 CTTCAAGATTGTTTGGAGCCTGAGGCGGAGCAGCAGCTGGCCAGACAGGCTCGGATGAA
  528 GCATGACATCATGTTCCAGCTGGAGTTCTTTATGCCCCTCGGCATCATCTTATTTTGCTC
   348 AGTGGTCCACCCCACCACGGGGTGAACACTATCTCCACCGGGTGGCGGCGGCTGGCATCGT
   408 CTGCACCCTGTGGCCCTGGTCATCCTGGGAACAGTGTATCTTTTGCTGGAGAACCATCT
  GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: NO. 6107475el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
   6300 Sears Tower, 233 South Wacker Drive
  ADDRESSEE: Marshall, O'Toole, Gerstein, Murray
ADDRESSEE: Borun
STREET: 6300 Sears Tower, 233 South Wacker Driv
  Sequence 43, Application US/09299843A Patent No. 6107475
  1576 CGACCCCATCATGTATTCTT 1596
   819 GGATCCCCTGGTGTATTT 839
   =
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   CITY: Chicago
STATE: Illinois
   Chicago
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1096 CATTGTGCACCCGGTCAAGTCCCTCAAGCTCCGCAGGCCCCTCTACGCACACCTGGCCTG 1155
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  48 GGTGATGCCGCCGCTGCTCATTGTGCCCTTTGTGCTGGCCGCACTAGGCAATGGGGTCGC 107
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  468 CTGCGTGCAAGAGGCGCCGTCTCCTGTGAGAGCTTCATCATGGAGTCGGCCAATGGCTG 527
   916 reresceeresceaerrerescerecrescerecrecrecececescerescrearr
  228 CAGACGTAGACACTGGGCTTTTGGGGACATTCCCTGCCGAGTGGGGCTCTTCACGTTGGC
  288 CATGAACAGGCCGGGAGCATCGTGTTCCTTACGGTGGTGGCTGCGGACAGGTATTTCAA
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6
   Length 1901;
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
   Score 109; DB 3; L
Pred. No. 6.6e-22;
0; Mismatches 415;
   RECISTRATION NUMBER: 43,213
REFERENCE/DOCKET NUMBER: 27866/32059B
REFERENCE/OCKET NUMBER: 27866/32059B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
  PRIOR SAFLICATION 1973

APPLICATION NUMBER: US 09/088,337
FILING DATE: 01-JUN-1998

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/153,848
FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Jill E. Uhl
   APPLICATION NUMBER: US/09/299,843A FILING DATE:
   MOLECULE TYPE: DNA (genomic)
   10.5%;
  SEQUENCE CHARACTERISTICS:
LENGTH: 1901 base pairs
  Best_Local Similarity 47.1
Matches 377; Conservative
  TELEX:
INFORMATION FOR SEQ ID NO:
  nucleic acid
EDNESS: single
  701..1717
  CLASSIFICATION: 435
   linear
  NAME/KEY: CDS
  STRANDEDNESS:
   US-09-299-843A-43
  TOPOLOGY:
  LOCATION:
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Query Match
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.276 TGCCCTGGTGTCCCTGGCAGTGGCCTTCACCTTCCCGTTCATCACCACGGTCACCTGCTA 1335
  CCTGCCCAGCGTGTCTGCTAGACTCTATTTCCTCTGGACGGTGCCCTCGAGTGCCTGCGA 758
   APPLICANT: Godiska, Ronald
Gray, Patrick W.
Schweikart, Vicki L.
TITLE OF INVENTION: NO. 6348574el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 66
  648 GAAGGCGACCCGGTTCATCATGTGGTGGCAATTGT-----GTTCATCATGCTA
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  528 GCATGACATCATGTTCCAGCTGGAGTTCTTTATGCCCCTCGGCATCATGTTTTGCTC
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  COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Tale PC COMPA:
COMPUTER: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/088,337B
FILING DATE: 01-Jun-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION DATE:
17-NOV-1993
APPLICATION NUMBER: US 08/153,848
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: US 07/977,452
  STREET: 6300 Sears Tower, 233 South Wacker Drive
   ADDRESSEE: Marshall, O'Toole, Gerstein, Murray
   FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
6348574and, Greta E.
REGISTRATION NUMBER: 35,302
   REFERENCE/DOCKET NUMBER: 31794
TELECOMMUNICATION INFORMATION:
   Application US/09088337B
  TELEFAX: (312) 474-0448
TELEX: 25-3856
   LENGTH: 1901 base pairs
   1576 CGACCCCATCATGTATTCTT 1596
   819 GGATCCCCTGGTGTATTT 839
  INFORMATION FOR SEQ ID NO: 43: SEQUENCE CHARACTERISTICS:
  TYPE: nucleic acid
STRANDEDNESS: single
  CORRESPONDENCE ADDRESS
   CITY: Chicago
STATE: Illinois
COUNTRY: USA
   (312)
  Sequence 43, Application Patent No. 6348574
GENERAL INFORMATION:
  ZIP: 60606
   US-09-088-337B-43
  669
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1216 CGTGCAGACCAACCACACGTGGTCTGCAGCTGTACCGGGAGAAGGCCTCCCACA 1275
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; SEQUENCE DESCRIPTION: SEQ ID NO: 43:
US-09-088-337B-43
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  10.5%;
ilarity 47.1%;
Conservative
TOPOLOGY: linear
   NAME/KEY:
                     MOLECULE TYPE:
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   PCT-US93-11153-43
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   APPLICANT: LI, VII.
APPLICANT: LI, VII.
APPLICANT: GOCANNE, JEANINE D.
APPLICANT: RUBEN, STEVEN M.
TITLE OF INVENTION: G-PROTEIN RECEPTOR HIBEB69
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: GARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
ADDRESSEE: GARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
ADDRESSEE: GENCRE FARM ROAD
CITY: ROSELAND
STATE: NJ
COUNTRY: NJ
COUNTRY: UJ
COUNTRY: GOGS
   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07180 FILING DATE: 06-JUNE-1995 CLASSIFICATION:
  ATTORNEY AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 30,073
REFERENCE/DOCKET NUMBER: 325800-366
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
  COMPUTER READBRE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
  Sequence 1, Application PC/TUS9507180 GENERAL INFORMATION:
   1576 cgaccccarcargrarrcrr 1596
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INFORMATION FOR SEQ ID NO: 1:
   SEQUENCE CHARACTERISTICS:
LENGTH: 2453 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Pred. No. 6.6e-22;
0; Mismatches 415; Indels
              APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: Novel Seven Transmembrane Receptors
NUMBER OF SOUTENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bickneil
STREET: 6300 Sears Tower, 233 South Wacker Drive
   COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/11153
FILING DATE:
  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
   NAME: Noland, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
TELECOMMUNICATION INFORMATION:
TELEFAN: (312) 474-6300
TELEFAN: (312) 474-6448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
  TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
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Best Local Similarity 47.1%;
Matches 377; Conservative
Godiska, Ronald
   LENGTH: 1901 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
  ; NAME/KEY: CDS
; LOCATION: 701..1717
PCT-US93-11153-43
  CITY: Chicago
STATE: Illinois
   CLASSIFICATION:
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421 TCTATGTTACCGTGCTGGTGGTGGCTTCCCGGCCAACTGCCTGTCCCTCTACTTCGGCT 480
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0; Mismatches 443;
                   NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road, P.O. Box 1539
  COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb
COMPUTER: IBM 486
  OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
   SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,974A
FILING DATE: October 3, 1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
  ATG50022
   34,344
   NAME: William T. Han
REGISTRATION NUMBER: 34,344
REFERENCE/DOCKET NUMBER: AT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610 270 5024
   10.0%;
Similarity 46.9%;
HUVCT36
  ATTORNEY/AGENT INFORMATION:
   TELEFAX: 610 270 5090 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 1597
   Conservative
  CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-0939
  Nucleic Acid
EDNESS: Single
 TITLE OF INVENTION:
  Linear
   STRANDEDNESS:
TOPOLOGY: Line
ANTI-SENSE: NO
   FILING DATE:
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Best Local Simmatches 399;
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  699 CCTGCCCAGCGTGTCTGCTAGACTCTATTTCCTCTGGACGGTGCCCTCGAGTGCCTGCGA
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   588 CTTCAAGATTGTTTGGAGCCTGAGGCGGAGCAGCTGGCCAGACAGGCTCGGATGAA
  9.
   Bergsma, Catherine E. Ellis
A No. 5912335el G-Protein Coupled Receptor
   Length 2453
   Score 109; DB 5; Length 24
Pred. No. 7.5e-22;
0; Mismatches 415; Indels
  Sequence 1, Application US/08724974A Patent No. 5912335 GENERAL INFORMATION:
APPLICANT: Derk J. Bergsma, Cathe TITLE OF INVENTION: A No. 5912335
  1423 CGACCCCATCATGTATTTCTT 1443
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   Query Match 10.5%;
Best Local Similarity 47.1%;
Matches 377; Conservative
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548..1564
                   NAME/KEY:
                                    LOCATION:
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TOPOLOGY:
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   961 GCATCCTGCGCGCGGTGCGCGGAGCCACGGCACCCAGAAGAGCCGCAAGGACCAGATCC 1020
  1021 Accederacrecaccaccarcarcrecrescerecrecerecrecereceraccacara 1080
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  776 CCCTGCACATAACCCTCAGCTTCACCTACATGAACAGCATGCTGGATCCCCTGGTGTATT
   APPLICANT: Lustig, Kevin D.
TITLE OF INVENTION: DNA Encoding the Human P2U Receptor and TITLE OF INVENTION: Null Cells Expressing P2U Receptors NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
FILING DATE: 16-MAY 1995 CLASSIFICATION: 435
  ADDRESSEE: Bell, Seltzer, Park & Glbson STREET: Post Office Drawer 34009 CITY: Charlotte STATE: No. 5596088th Carolina COUNTRY: USA
  NAME: Sibley, Kenneth D. REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5470-71A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-420-2200
  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
  Sequence 1, Application US/08442134A
Patent No. 559608B
GENERAL INFORMATION:
APPLICANY: Boucher, Richard C.
   Boucher, Richard C.
Weisman, Gary A.
Turner, John T.
Harden, Thomas K.
Parr, Claude E.
Sullivan, Daniel M.
   INFORMATION FOR SEQ ID NO: 1:
   CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
  SEQUENCE CHARACTERISTICS:
LENGTH: 1842 base pairs
   919-881-3175
  TYPE: nucleic acid
STRANDEDNESS: single
   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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APPLICANT:
  08-442-134A-1
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  DNA Encoding the Human P2U Receptor
Null Cells Expressing P2U Receptors
   Indels
   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
  0; Mismatches 204;
   8.9%; Score 92.6; DB 1;
  ADDRESSEE: Bell, Seltzer, Park & Glbson STREET: Post Office Drawer 34009 CITY: Charlotte STATE: No. 5607836th Carolina COUNTRY: USA
  Pred. No.
  APPLICATION NUMBER: US/08/444,581B
FILING DATE: 19-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
  Sequence 1, Application US/08444581B Patent No. 5607836
  Turner, John T.
Harden, Thomas K.
Parr, Claude E.
Sullivan, Daniel M.
   APPLICANT: Erb, Laura
APPLICANT: Lustig, Kevin D.
TITLE OF INVENTION: DNA Encod
TITLE OF INVENTION: Null Cell
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
  Boucher, Richard
Weisman, Gary A.
   51.3%;
  CURRENT APPLICATION DATA:
   Best_Local Similarity 51.39
Matches 215; Conservative
  57..1181
MOLECULE TYPE: CDNA
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APPLICANT:
APPLICANT:
   NAME/KEY:
LOCATION:
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APPLICANT:
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  US-08-442-134A-1
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0; Mismatches 204; Indels 0
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TELEPHONE: 919-881-3175
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1842 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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TOPOLOGY: Linear
   US 08/442,134
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Best Local Similarity 51.3%;
Matches 215; Conservative (
APPLICATION NUMBER: US 06
FILING DATE: 16-MAY-1995
ATTORNEY/AGENT INFORMATION:
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57..1181
   ; NAME/KEY:
; LOCATION:
US-08-444-581B-1
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Search completed: October 29, 2002, 02:43:00 Job time : 71 secs

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MEDLINE=21458557; PubMed=11574155;
Lee D.K., Vanti W.B., Arkhitko O.,
Lewis T., Evans J.F., George S.R., O'Dowd B.F.;
"Discovery and mapping of ten novel G protein-coupled receptor
  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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   Wang Y.-g, Gong L.;
"Molecular cloning of FKSG80, a novel gene encoding a putative
chemokine receptor.";
   01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PUTATIVE CHEMOKINE RECEPTOR (G PROTEIN-COUPLED RECEPTOR).
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Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases
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  genes,";

Gene 275:83-91(2001).

EMBL; AF411110; AAL26481.1; -.

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HSSP; P34996; 1DDD.

InterPro; PR000276; GPCR_Rhodpsn.

Pfam; PF00001; 7tm.1; 1.

PRINTS; PR00237; GPROTEIN.RECEP_F1_1; UNKNOWN_1.

PROSITE; PS500237; G_PROTEIN.RECEP_F1_2; 1.
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SEQUENCE
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   29BXC0;
   Q9BXC0
   Q9hcq2 homo sapien
Q9ns75 homo sapien
Q95n03 sus scrofa
Q92419 rattus norv
Q9de05 raja erinac
Q9us77 xenopus lae
Q9ue21 homo sapien
Q9udz6 homo sapien
   O9bxcO homo sapien
O9ep66 mus musculu
O9nG2O homo sapien
O9jls1 mus musculu
O920al mus musculu
   Q9dgq6 carassius a Q9cpz4 mus musculu Q96em8 homo sapien
   October 29, 2002, 03:50:26; Search time 69 Seconds (without alignments) 867.482 Million cell updates/sec
   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
   346
   Description
  US-09-886-041-2
1853
1 MYNGSCCRIEGDTISQVMPP.....ANSFQSQSDGQWDPHIVEWH
                       GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
  fotal number of hits satisfying chosen parameters:
   562222 seqs, 172994929 residues
  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
  OM protein - protein search, using sw model
   Q9BXC0
Q9EP66
Q9NQ20
Q9JLS1
Q9JLS1
Q9HCQ2
Q9HCQ2
Q9NS75
Q9SN03
Q924T9
Q924T9
   Q9DGQ6
Q9CPZ4
Q96EM8
  BLOSUM62
Gapop 10.0 , Gapext 0.5
  4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
   sp_unclassified:*
   sp_rodent:*
sp_virus:*
sp_vertebrate:*
   sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
   sp_archea:*
sp_bacteria:*
  Minimum DB seq length: 0
Maximum DB seq length: 200000000
   13 13 13
  13
   Length DB
  sp_plant:*
   sp_fung1:*
   SPTREMBL_19:*
  sp_phage: *
  Match
  100.0
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   Query
   1853
868.5
446.5
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371.5
366.5
365.5
342.5
341
  336
334
329.5
317
310
  Perfect score:
  Scoring table:
   Score
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Score 1853; DB 4; Length 346;

100.08;

Query Match

Result

Q9epp3 cavia porce Q9epp8 homo sapien Q99mt7 mus musculu Q9qw32 rattus sp. Q9jk47 mus musculu Q9eqr9 meriones un Q9jly8 rattus norv Q9by21 homo sapien Q924t8 rattus norv

Q9gln9 pan troglod Q96jz8 homo sapien

Q9byx5 homo sapien Q964d4 periplaneta Q9jj71 mus musculu

241

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250 RIFWLLYKYNVRNCDIYSSVDLAFFTTLSFTYMNSMLDPVVYYFSSPSFPNFFSTCINRC 309
   67 CLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNT 126
   66 CLPFLAAFYLSLQAWHLGRVGCWALHFLLDLSRSVGMAFLAAVALDRYLRVVHPRLKVNL 125
   182 OLEFFMPLGIILFCSFKIVWSLRRR-QQLARQARMKKATRFIMVVAIVFITCYLPSVSAR 240
   127 ISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANG-----WHDIMF 181
  6 CSAPSTVVATAVGVLLGLECGLGLIGNAVALWTFLFRVRVWKPYAVYLLNLALADLLLAA 65
  7 CRIEGDIISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMI 66
   242 YELWTVPS---SACD--PSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICS
  HAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIMF
  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
   241 --LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKL 292
  Length 319;
   243 VLMHIFQNLGSCRALCAVAHTSDVTGSLTYLHSVLNPVVYCFSSPTFRSSYRRV
   Indels
  Almeida J.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
PRINITS; PR00237; GPRRDDOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
   319 AA; 35074 MW; 2ACD0350AD7FB53A CRC64;
  01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
BAS17H2.2 (G PROTEIN-COUPLED RECEPTOR 31).
   24.3%; Score 450.5; DB 4;
llarity 34.4%; Pred. No. 6e-37;
Conservative 61; Mismatches 121;
  Ź
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   319
   PRT;
  PRT;
   LKPKQPGHSKTQRPEEMPIS 316
   310 LRKKTLGEPDNNRSTSVELT 329
  PRELIMINARY;
   PRELIMINARY;
   Similarity
  [1]
SEQUENCE FROM N.A.
  NCBI_TaxID=9606;
  Best Local Sim
Matches 101;
  Receptor.
SEQUENCE
  Query Match
   Q9JLS1
Q9JLS1;
                       122
  RESULT 4
Q9JLS1
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  DFLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHP 120
  HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIM 180
   FQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSAR 240
   LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK 300
  FLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPH 121
  a novel
                          Gaps
  MYNGSCCRIEGDIISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVA 60
  Gaps
  NG-SCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVAD 61
  STRAIN-129/SVJ, AND C57BL/6; Schaub A., Futterer A., Pfeffer K.; Schaub A., Futterer A., Pfeffer K.; PUMA-6, an interferon-gamma inducible gene in macrophages is a novement of the seven transmembrane spanning superfamily."; Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
--- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
--- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS. EMBL; AJ300199; CAC17791.1; ---
EMBL; AJ300199; CAC17791.1; ---
HSSP: P34996; 1DDD.
   Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
  roprotein; Receptor; Transmembrane CCCE52A2475777FC CRC64;
   7;
                       ;
0
   DB 11; Length 360;
  46.9%; Score 868.5; DB 11; Length
55.6%; Pred. No. 9.3e-79;
.ive 39; Mismatches 96; Indels
                          Indels
   01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PUTATIVE SEVEN TRANSMEMBRANE SPANNING RECEPTOR.
PUMAG OR PUMA-G.
  Pred. No. 2.2e-177;
                            ö
  360 AA
  MGD; MGI:193333; Pumag.
InterPro; IPR000276; GFCR_Rhodpsn.
PRO0001; 7tm_1; 1.
PROSTIE; PR000237; GPROTEIN_RECEP_FI_1; 1.
PROSTIE; PS00237; G_PROTEIN_RECEP_FI_2; 1.
G_PROTEIN, RECEP_FI_2; 1.
SEQUENCE 360 AA; 41400 MW; CCCE52A24757
                     Mismatches
  PRT;
                     ő
   Mus musculus (Mouse)
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
100.0%;
  Best Local Similarity 55.6*
Matches 178; Conservative
                       Matches 346; Conservative
  PRELIMINARY;
Best Local Similarity
   SEQUENCE FROM N.A.
  NCBI_TaxID-10090;
  Query Match
  Q9EP66
Q9EP66;
  241
  --
  62
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   RESULT 2
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Cyslt2.";
  SEQUENCE FROM N.A.
   CYSLTR-LIKE
      receptor, Submitted
   Receptor.
SEQUENCE
   SEQUENCE
  Query Match
   Receptor
   Suga H.;
   09HCQ2;
   Matches
  127
   RESULT 6
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  182 QLEFFMPLGIILFCSFKIVWSLRRR-QQLARQARMKKATRFIMVVAIVFITCYLPSVSAR 240
  241 --LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLK 298
  :: | : :: | | : :: | | : :: | | :: | | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | ::
   CLPFRIDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNT 126
  127 ISTRVAAGIVCTLWALVILGTVYLLLENHLC-VQETAVSCESFI----MESANGWHDIMF 181
   6 CSAASTVVETAVGTMLTLECVLGLMGNAVALWTFFYRLKVWKPYAVYLFNLVVADLLLAT 65
   Gaps
  CRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMI 66
   Mus musculus (Mouse).
Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
   mouse
  19;
  DB 11; Length 319;
   Hul Y., Funk C.D.; Molecular cloning of the murine cysteinyl leukotriene type
   the
  24.1%; Score 446.5; DB 11; Length 32.5%; Pred. No. 1.5e-36; ive 64; Mismatches 133; Indels
   Schimenti J.C.; "ORFless, and mutant transcription units in
  SEQUENCE 319 AA; 35551 MW; 571F6DFB485BD7C4 CRC64;
   01-DEC-2001 (TTEMBLrel. 19, Created)
01-DEC-2001 (TTEMBLrel. 19, Last sequence update)
01-DEC-2001 (TTEMBLrel. 19, Last annotation update)
01-DEC-2001 (TTEMBLREL. 19, Last annotation update)
CYSTEINYL LEUKOTRIENE RECEPTOR TYPE 2.
                         Last sequence update)
Last annotation update)
  complex responder (Tcr) locus.";
Mamm. Genome 10:869-976(1999).
Mambl., AF14/008; AR726668.1; -.
MGD; MGI:9843; Tcpl0c.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7rm_1; 1.
PRINTS; PR000237; GPCRRHODOPSN.
PROSITE; PS500237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
PROSITE; PS500262; G_PROTEIN_RECEP_F1_2; 1.
  309 AA
    Created)
   PRT;
  MEDLINE-99431663; PubMed-10501965;
  299 PKQPGHSKTQRPEEMPISNL 318
   GR-----RKAAESPSDNL 314
01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TREMBLRel. 15, 01-JUN-2011 (TREMBLREL. 17, G PROTEIN COUPLED RECEPTOR. TCP10C.
  Matches 104; Conservative
   PRELIMINARY;
  Mus musculus (Mouse).
   Similarity
  SEQUENCE FROM N.A.
   SEQUENCE FROM N.A.
  NCBI_TaxID=10090;
   TISSUE-HEART;
  Receptor.
  Query Match
   Best Local
  0920A1
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   RESULT 5
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  59 VADFLLMICLPFRTDYYLRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVV 118
   119 HPHHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSC-----ESFIMESA 173
   | | : | | : | | : | : | : | | : | HPFRMFHVTSVR-SAMILCGIIWVFIMASSALLLVNGQEEKDNIISCLELSPQKF--KSL 182
  60 ADFILMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVH 119
  SULLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNWYSSIYFLTVLSVVRFLAWVH 126
   120 PHHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSC---ESFIMESANGW 176
  174 NGWHDIMFQLEFFWPLGIILFCSFKIVWSLRRRQ--QLARQARMKKATRFIMVVAIVFIT 231
   Gaps
  Gaps
   2 YNGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPST---VYLFNLA 58
  3 NGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPST---VYLFNLAV 59
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
  "Homo saplens cystelnyl leukotriene receptor 1 like receptor."; Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AB041644; BAB16379.11; -.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_l; 1.
PRIMTS; PR00237; GPCRRHODOPSN.
PROSSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
  DB 4; Length 330;
   CYLPSVSARLYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSF
  DB 11; Length
   20.0%; Score 371.5; DB 11; Length 32.7%; Pred. No. 4.7e-29; ive 56; Mismatches 125; Indels
   19.8%; Score 366.5; DB 4; Length 29.9%; Pred. No. 1.6e-28; Live 69; Mismatches 134; Indels
(DEC-2000) to the EMBL/GenBank/DDBJ databases
   330 AA; 37784 MW; 4C34CC4A8DD13EB4 CRC64;
   309 AA; 35227 MW; 327B14A6EDDD2A02 CRC64;
   01-WAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CYSTEINYL LEUKOTRIENE RECEPTOR LIKE RECEPTOR.
   PRT;
                       EMBL; AF331658; AAK97354.1;
   Query Match
Best Local Similarity 32.7%
   Local Similarity 29.99
   PRELIMINARY;
  Homo sapiens (Human).
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Query Match
   Best Local
Matches 8
   CYSLT2.
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  TISSUE-PLACENTA;
MEDLINE-20374466; PubMed-10913337;
Taksasui J., Kamohara M., Matsumoto M., Saito T., Sugimoto T., Ota T.,
Nishikawa T., Kawai Y., Masuho Y., Isogai T., Suzuki Y., Sugano S.,
  Helse C.E., O'bowd B.F., Figueroa D.J., Sawyer N., Nguyen T., Im D.S., Stocco R., Bellefeuille J.N., Abramovita M., Cheng R., Williams D.L. Jr., Zeng Z., Liu Q., Ma L., Clements M.K., Coulombe N., Liu Y., Austin C.P., George S.R., O'Neill G.P., Metters K.M., Lynch K.R., Evans J.F., "Characterization of the homan cysteinyl leukotriene Z receptor."; J. Biol. Chem. 275:30531-30336(2000).
  PSVSARLYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKI 294
  HDIMFQLEFFMPLGIILFCSFKIVWSLRRRQ--QLARQARMKKATRFIMVVAIVFITCYL 234
   Furuichi K.; "The molecular characterization and tissue distribution of the human
   a Second
                             Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
  19.8%; Score 366.5; DB 4; Length 346; 29.9%; Pred. No. 1.7e-28; ive 69; Mismatches 134; Indels 17;
   01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 19, Last annotation update)
CYSTEINYL LEUKOTRIENE CYSLT2 RECEPTOR (BA108P5.1) (CYSTEINYL
BA108P5.1 OR CYSLT2.
   Nothacker H.-P., Wang Z., Zhu Y., Civelli O.;
"Identification, Molecular Cloning and Characterization of Human Cysteinyl Leukoriene Receptor.";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AR018269; BAB03601.1;
EMBL; AR254664; AAG17281.1;
EMBL; AR279611; AAK69485.1;
  Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases
   39635 MW; EB54A4A2DDCE5EE4 CRC64;
   cysteinyl leukotriene CysLT2 receptor.";
Biochem. Biophys. Res. Commun. 274:316-322(2000).
   346 AA
  PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
   InterPro; IPR004071; Cysleuk_receptor.
InterPro; IPR000276; GPCR_Rhodpsn.
   PRT;
  PRINTS; PR01533; CYSLTRECPTR.
PRINTS; PR00237; GPCRRHODOPSN.
   PRELIMINARY;
  295 CSLKPKQPGHSKTQ 308
   302 SALRKGHPQKAKTK 315
   Pfam; PF00001; 7tm_1;
   346 AA;
   SEQUENCE FROM N.A.
  SEQUENCE FROM N.A.
   SEQUENCE FROM N.A.
   SEQUENCE FROM N.A.
  NCBI_TaxID=9606;
   PubMed-10851239
   SEQUENCE
   Query Match
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   Dunn M.
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120 PHHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSC---ESFIMESANGW 176
   202 NYIALVVGCLIPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALFTIITLIIFFLCFL 261
   SEQUENCE FROM N.A. Katsumoto M., Matsumoto S., Saito T., Kamohara M., Takasaki J., Matsumoto M., Matsumoto T., Matsushime H., Furuichi K.; Obishi T., Soga T., Matsushime H., Furuichi K.; Characterization of the cloned rat and porcine cysteinyl leukotriene
   LFCSFKIVWSLRRRQQLARQARM--KKATRFIMVVAIVFITCYLPSVSARLYFLWTVPSS 250
  ADFLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVH 119
   143 PFRLLHVTSIR-SAWILCGIIWILIMASSIMLLDSGSEQNGSVTSCLELNLYKIAKLQTM 201
  234
  PSVSARLYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKI 294
   LRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNTISTRVAAGI 135
   136 VCTLWALVILGTVYLLLENHLCVQETAVSC---ESFIMESANGWHDIMFQLEFFMPLGII 192
59
   Gaps
  19 PPLLIVAFVLGALGNGVALCGFCFHMKTWKPST - - - VYLFNLAVADFLLMICLPFRTDYY 75
  27 NSRNCTIE-NPKREFFPIVYLIIFFWGVLGNGLSIYVF---LQPYKKSTSVNVFMLNLAI
   43 PIVYLVIFIWGALGNGFSIXVF---LKPYKKSTSVNVFMLNLAISDLLFTITLPFRVDXY
     NGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPST---VYLFNLAV
  HDIMFOLEFFMPLGIILFCSFKIVWSLRRRQ--QLARQARMKKATRFIMVVAIVFITCYL
  Euteleostomi;
Sus.
   12;
  19.5%; Score 362; DB 6; Length 345; 31.3%; Pred. No. 4.8e-28; Live 59; Mismatches 118; Indels
   to the EMBL/GenBank/DDBJ databases
  receptors.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ database:
EMBL; AB052662; BAB60817.1; -
SEQUENCE 345 AA; 39410 MW; 5D1B1FB89BB95905 CRC64;
  Chordata; Craniata; Vertebrata;
Cetartiodactyla; Suina; Suidae;
  Last sequence update)
Last annotation update)
  ACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSF 285
  279 KCKDRLHKAVAVTLALAAANSCFNPFLYYFAGENF 313
  345 AA
   Created)
   PRT;
   (TrEMBLrel. 19, C
(TrEMBLrel. 19, I
(TrEMBLrel. 19, I
  86; Conservative
  PRELIMINARY;
   295 CSLKPKQPGHSKTQ 308
   318 SALRKGHPOKAKTK 331
   Sus scrofa (Pig).
Eukaryota; Metazoa;
Mammalia; Eutheria;
   Similarity
  NCBI_TaxID=9823;
   01-DEC-2001 (01-DEC-2001 (01-DE
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Pfam; PF00001; 7tm_1; 1
   93;
   Receptor.
SEQUENCE
  SEQUENCE
  Query Match
  Q90X57;
  Local
   Q90x57
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   Matches
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  SEQUENCE FROM N.A.
Kamohara M., Takasaki J., Matsumoto M., Matsumoto S., Saito T.,
Ohishi T., Soga T., Matsushime H., Furuichi K.;
"Characterization of the cloned rat and porcine cysteinyl leukotriene
  119 HPHHAVNTISTRVAAGIVC-TLWALVILGTVYLLLENHLCVQETAVSCESFIMESAN--G 175
  59 VADFLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVV 118
   176 WHDIMFQLEFFMPLGIILFCSFKIVWSLRRRQ--QLARQARMKKATRFIMVVAIVFITCY 233
  Rattus norvegicus (Rat).
Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
  Gaps
   2 YNGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPST---VYLFNLA 58
  Raja erinacea (Little skate).
Eukaryota, Metazoa, Chordata; Craniata, Vertebrata; Chondrichthyes;
Elasmobranchii; Squalea; Hypnosqualea; Pristiorajea; Batoidea;
Rajiformes; Rajidae; Raja.
NCBI_TaxID=7782;
   MEDLINE-20151: PubMed-10900200;
Dranoff J.A., O'Nelll A.F., Franco A.M., Cai S.Y., Connolly G.C.,
Ballatori N., Boyer J.L., Nathanson M.H.;
A printitive ATP receptor from the little skate Raja erinacea.";
J. Blol. Chem. 275:30701-30706(2000).
EMBL; AF242850; AAG42684.1;
HSSP; P34996; 1DDD.
InterPro; IPR000276; GPCR_Rhodpsn.
   13;
   DB 11; Length 309;
   234 LPSVSARLYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSF 285
  57; Mismatches 131; Indels
   receptors.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
EMBL: AB052661; BAB60816.1; '.
SEQUENCE 309 AA; 35507 MW; A122AC8177879D56 CRC64;
  01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
  Last sequence update)
Last annotation update)
   19.2%; Score 355.5; DB 1
31.2%; Pred. No. 1.9e-27;
   309 AA
  357
  Created)
   PRT;
  PRT;
   (TrEMBLrel. 19, C
(TrEMBLrel. 19, I
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  91; Conservative
  PRELIMINARY;
   PRELIMINARY;
  Local Similarity
   SEQUENCE FROM N.A.
   P2Y RECEPTOR.
   01-DEC-2001 (
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   TISSUE-LIVER
   Query Match
   0924T9
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  Matches
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78 RRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNTISTRVAAGIVC 137
  138 T-LWALVILGTVYLLL-----ENHLCVQETAVS-CESFIMESANGWHDIMFQLEFF 186
  MPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLP----SVSA 239
   RRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNTISTRVAAGIVC 137
   KTDWIFGDALCKLORFLFHVNLYGSILFLTCISVHRYTGVVHPLKSLGRLKKKNSIYISA 161
  138 TLWALVILGTVYLLLENHLCVQET-AVSC------ESFIMESANGWHDIMFQLEFFM 187
   97
   Gaps
   18 MPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMICLPFRTDYYLR 77
   18 MPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMICLPFRTDYYLR 77
  212 IPFATILVCYGFIVKALISNDM--KTPLRGKSVRLVIIVLAVFAISYLPFHVMKNLNLQS
   RLYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKL--KICSL
   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
   18.5%; Score 342.5; DB 13; Length 357; 26.4%; Pred. No. 4.5e-26; Live 69; Mismatches 144; Indels 29;
   Length 361;
   Indels
   Cheng A.W., Tsim K.W.; "Cloning of Xenopus P2Yl Receptor."; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases EMBL; AF432354; AAL27614.1; -.
   361 AA; 41002 MW; E5B2D605F5B57FED CRC64;
   41239 MW; 14604EE15DCBDB41 CRC64;
   (TrEMBLrel. 19, Created)
(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOMN_1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
   18.4%; Score 341; DB 13;
29.0%; Pred. No. 6.4e-26;
tive 61; Mismatches 135;
   Ā
   361
   298 KPKQPGHSKTQRPEEMPISNLGRRSCISV 326
   329 RSELSMOFRSEDSPLOPVSNISONGDTSL 357
   Xenopus laevis (African clawed frog).
   87; Conservative
   Conservative
  P2Y1 NUCLEOTIDE RECEPTOR.
   PRELIMINARY;
   Xenopodinae; Xenopus
  357 AA;
  Query Match
Best Local Similarity
Matches 87; Conserv
  Similarity
   SEQUENCE FROM N.A.
   NCBI_TaxID=8355;
   01-DEC-2001
01-DEC-2001
01-DEC-2001
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86 IPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNTISTR--VAAGIVCT-LWAL 142
   MEDLINE-20453044; PubMed-10996426;
Lin X., Janovick J.A., Cardenas R., Conn P.M., Peter R.E.;
"Molecular cloning and expression of a type-two somatostatin receptor
in goldfish brain and pituitary.";
  L--HITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPKQPGHSKTQRPEEMPIS 316
   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes; Cyprinidae; Carassius.
  26 FVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMICLPFRTDYYLRRRHWAFGD
  | ||: | : | : | | | | | | | | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 
   143 VILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIMFQLEFFMPLGIILFCSFKIVWS
   LRRRQQLARQARMK-KATRFIMVVAIVFITCYLP-SVSARLYFL-WTVPSSACDPSVHGA
   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
   298 AA; 33397 MW; 36DAD60B157B9EDB CRC64;
  SEQUENCE FROM N.A.
Blaesius R.H., Weber R.G., Lichter P., Ogilvie A.;
Blaesius R.H., Weber R.G., Lichter P., Ogilvie A.;
A novel Crphan G-protein coupled receptor primarily
brain is localized on human chromosomal band 2q21.";
J. Neurochem. 1998:1357-1365(1998).
BEMBJ. SLA55; CAB08108.1;
HSSP; P34996; 1DDD.
  Last sequence update)
Last annotation update)
  Last sequence update)
   Interpro: IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRRHODPSN.
PROSITE: PS00237; G_PORTEIN_RECEP_F1_1; UNKNOWN_1.
PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1.
Roceptor; G_Protein coupled receptor.
RON_TER
SEQUENCE 298 AA; 33397 MW; 36DAD60B157B9EDB CR
  Query Match 18.0%; Score 334; DB 4; Le
Best Local Similarity 31.8%; Pred. No. 2.6e-25;
Matches 95; Conservative 50; Mismatches 140;
   01-MAY-2000 (TrEMBLE1. 13, Greated)
01-MAY-2000 (TrEMBLE1. 13, Last sequence update)
01-JUN-2001 (TrEMBLE1. 17, Last annotation update)
02Y-LIKE G-PROTEIN COUPLED RECEPTOR (FRAGMENT).
298
   380
  01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last ann
SOMATOSTATIN RECEPTOR TYPE TWO.
PRT;
   PRT;
   Carassius auratus (Goldfish).
PRELIMINARY;
   PRELIMINARY;
   SEQUENCE FROM N.A.
  NCBI_TaxID=9606;
  NCBI_TaxID=7957;
  TISSUE-BRAIN;
   905060
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   A Blacelus R.H., Weber R.G., Lichter P., Ogilvie A.;

"A novel orphan G-protein coupled receptor primarily expressed in the brain is localized on human chromosomal band 2q21.";

"A novel orphan G-protein coupled receptor primarily expressed in the brain is localized on human chromosomal band 2q21.";

"I Neurochem. 1998:1357.1365(1998).

"EMBL; Y12546; CAA73144.1;

"R HSSP; P34996; IDDD.

"R HSSP; P34996; IDDD.

"R FINTER: PRO0001; 7tm_1, 1.

"R PROSTIE; PS0000237; GPCRRHODOPSN.

"R PROSTIE; PS000237; GPCRRHODOPSN.

"R PROSTIE; PS000237; GPROTEIN_RECEP_FI_2; 1.

"R PROSTIE; PS000237; GPROTEIN_RECEP_FI_2; 1.

"R RECEPTOR: G-protein coupled receptor.

"R RECEPTOR: 367 AA; 40989 MW; 132FBE97BE83C60C CRC64;
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  167
  227
  217 PFILILGCYGLIVRALIYKDMNNAPLR-KKSIYLVIIVLTVFAVSYLPFHVMKNLNLRAR 275
   | | : : :: |:| :| :| :| :| CQQETPLENMLFASFYLLDFILALVGNTLALWLFIRDHKSGTPANVFLMHLAVADLSCVL 110
  CLPFRTDYYLRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNT 126
   ISTR--VAAGIVCT-LWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIMFQL 183
   Gaps
   CRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMI 66
   228 AFTFPFITTVTCXLLIRSL--RQGLRVEKRLKTKAVRMIAIVLAIFLVCFVPYHVNRSV
   LKLRRPLYAHLACAFLWVVVAVAMAPLLVSPQTVQTNHTVVCLQLYREKASHHALVSLAV
   EFFMPLGIILFCSFKIVWSLRRRQQLARQARMK-KATRFIMVVAIVFITCYLP-SVSARL
  YFL-WTVPSSACDPSVHGAL--HITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLK
   241 LYFLWTVPSSAC - - DPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLK
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  14;
  18.1%; Score 336; DB 4; Length 367; 30.5%; Pred. No. 2.1e-25;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
   Indels
                          PLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLP-
   Last sequence update)
Last annotation update)
  153;
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  Mismatches
   367
  01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last seq
01-JUN-2001 (TrEMBLrel. 17, Last ann
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   54;
   330 ASRRSEANVQSKSEEVTLNIL 350
   299 PKQPGHSKTQ-RPEEMPISNL 318
  PKQPGHSKTQRPEEMPIS 316
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   Conservative
   PRELIMINARY;
   Homo sapiens (Human)
  Similarity
  SEQUENCE FROM N.A.
   NCBI_TaxID-9606
   97;
  Query Match
  Local
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Best Loc Matches

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Gaps 85 9

Length 298;

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Q9UE21; **Q9UE21** 

RESULT 12

**Q9UE21** 

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   STRAIN-CSTBL/63; TISSUE-HEAD, AND LIVER;

X RAWAI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

X Arakawa T., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Sabburner M., Batalov S., Casavant T.,

Radota K., Matsudi F., Suzuki R., Tomita M., Wagner L., Washio T.,

Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Sakai K., Okido T., Furuno M., Anno H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Blake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N. H.,

Nordone P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

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Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

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Nyashizaki Y., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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  168 KSISLAMWVISLLVNLPIMIYSGVNVKKNEARTCTMLMPEPQNTYYTVFIFYTFFMGFFL 227
  PLIVICMCYLLIVIKVKSSGMRVCSSKRKRSERKVTRMVSIVVVVVVVLVLCWLPFXVFNVTS 287
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PROSTITE: PS00237; GPCRRHODOPSN.
PROSTITE: PS00237; GPCRRHODOPSN.
PROSTITE: PS02625; G_PROTEIN_RECEP_F1_1; 1.
G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Endocrinol. 166:75-87(2000)
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   SEQUENCE FROM N.A.
  Hayashizaki Y.;
   Match
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Best Local
  09CPZ4;
  09CPZ4
   288
  Matches
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  09CPZ4
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64 LMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHA 123
  82 YAASLPLLVYYYARGDHWPFSTVLCKLVRFLFYTNLYCSILFLTCISVHRCLGVLRPLHS 141
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   227 IVFITCYLP-SVSARLYFLWTVPSSACDP--SVHGALHITLSFTYMNSMLDPLVYYFSSP 283
  252 AVFALCFLPFHLTRTLYYSFRSLDLSCHTLNAINMAYKITRPLASANSCLDPVLYFLAGG 311
  Gaps
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  Length 373;
  Indels
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EMBL; AK055013; BAB23746.1; -.
HSSP; PA$96; IDDD.
MGD; MG1:105107; PZY2.
InterPro; IPR000276; GPCR_Rhodpsn.
PRINTS; PR00237; GPCRHODPSN.
PROSITE; PS00237; GPROTEIN_RCCEP_FI_1; UNKNOWN_1.
PROSITE; PS00262; G_PROTEIN_RCCEP_FI_2; 1.
SEQUENCE 373 AA; 42188 MW; E4BD653D895DCE8F CRC64;
  Query Match 17.1%; Score 317; DB 11; Best Local Similarity 29.8%; Pred. No. 1.7e-23; Matches 97; Conservative 45; Mismatches 150;
  Search completed: October 29, 2002, 04:54:31
Job time : 75 secs
  284 SFPKFYNKLKICSLKPKQPGHSKTQR 309
   RLVRFARDAK ---- PPTEPTPSPQAR 333
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   19-DEC-2001
  04-OCT-2001
  105.8
105.8
104.2
104.2
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  Key
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Human nGPCR11 codi
Human GPCR12 polyn
Human GPCR12 polyn
Human G-protein co
cDNA encoding HM74
Gene encoding nove
Human GPCR1c polyn
  cDNA encoding nove
  October 29, 2002, 00:07:23 ; Search time 209 Seconds (without alignments) 8551.713 Million cell updates/sec
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   1 atgtacaacgggtcgtgctg.....acattgttgagtggcactga 1041
  Description
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd
   Total number of hits satisfying chosen parameters:
   1736436 seqs, 858457221 residues
  SUMMARIES
   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
  AAS07946
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ABA81529
ABA81530
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AAS18501
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ABA81531
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  AAS12581
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Gapop 10.0 , Gapext 1.0
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   seq length: 0
seq length: 2000000000
  8
   US-09-886-041-1
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1730
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   Score
  Perfect score:
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Human cell surface
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Human G-protein co
NA encoding human
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Human R12 seven tr
Human G-protein th
DNA encoding human
   Human opioid-type
Human 7TM clone HE
cDNA clone HEOAD54
Human DNA for pote
   DNA encoding human
Sequence of orphan
Human DNA for pote
Human cDNA encodin
                                    Human cDNA encodin
  Human G protein-co
DNA encoding novel
DNA encoding novel
  Human G protein-co
  Human nGPCR11 cod:
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  27-MAR-2000; 2000US-192419P.
06-SEP-2000; 2000US-230459P.
20-SEP-2000; 2000US-0666535.
   27-MAR-2001; 2001WO-US09522
   (first entry)
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  601
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   661
   721
  781
  841
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   The present invention relates to the isolation of a novel human G-protein coupled receptor (GPCR) which is related to the chemokine receptor subfamily. The CDNA and gene sequences encoding for GPCR are also given in the invention. The sequences of the invention are useful for diagnosing and treating diseases or conditions mediated by human proteins are sequences of the invention are useful.

Co diagnosing and treating diseases or conditions mediated by human proteins are sequences of conditions mediated by human ce groundly and protein in inflammatory disorders.

Ce.g. hyperplasia), neurological disorders (e.g. parkinson's disease), psychiatric diseases (e.g. schizophrenia), inflammatory disorders or e.g. adult respiratory disorders or distress syndrome, ARDS). The GPCR protein is also useful for identifying a modulator of the expression of the protein. It also serves as a target for identifying agents for use in mammalian therapeutic applications, ce.g. a human drug, particularly modulating a biological or pathological response in a cell or tissue that expresses the protein, in biological response in a cell or tissue that expresses the protein, in biological sequence related to GPCRs that are related to members of the chemokine receptor subfamily, in drug screening assays and in competition binding assays. GPCR is also useful in diagnosing a disease or predisposition to a disease mediated by the peptide, in pharmacogenomic analysis. The control of the novel human GPCR of the invention.
   ö
  Novel human G-protein coupled receptor proteins and nucleic acid molecules encoding the protein for use in developing human therapeutics and diagnostic compositions and for identifying modulators of the
   360
   420
  480
  CTGCTCATTGTGGCCTTTGTGCTGGGCGCACTAGGCAATGGGGTCGCCCTGTGTGGTTTC 120
   240
  300
  300
   360
   CTGCTCATTGTGGCCTTTGTGCTGGGCGCACTAGGCAATGGGGTCGCCCTGTGTGGTTTC 120
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                     Beasley
                     Di Francesco V,
  Claim 23; Fig 1; 66pp; English.
   Best Local Similarity 100.
Matches 1041; Conservative
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   361
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G protein-coupled receptor; nGPCR; seven transmembrane receptor; signal transduction; schizophrenia; thyroid disorder; renal failure; rheumatoid arthritis; CNS disorder; infection; metabolic disease; cardiovascular disease; proliferative disorder; hormonal disorder; neurological disorder; neuronal disorder; Alzheimer's disease; attention deficit-hyperactivity disorder/attention deficit disorder; Parkinson's disease; migraine; senile dementia; inflammatory disease;
  AGGAGTTGCATCAGTGTGGCAAATAGTTTCCAAAGCCAGTCTGATGGGCAATGGGATCCC 1020
   TTCATCATGGTGGTGGCAATTGTGTTCATCACATGCTACCTGCCCAGCGTGTCTGCTAGA
   TCAAGCCCCTCCTTTCCCAAATTCTACAACACGCTCAAAATCTGCAGTCTGAAACCCAAG
  901 CAGCCAGGACACTCAAAAACACAAAAGGCCGGAAGAGATGCCAATTTCGAACCTCGGTCGC
            GCCCTGGTCATCCTGGGAACAGTGTATCTTTTGCTGGAGAACCATCTCTGCGTGCAAGAG
  TICATCATGGTGGTGGCAATTGTGTTCATCACATGCTACCTGCCCAGCGTGTCTGCTAGA
   CTCTATTTCCTCTGGACGGTGCCCTCGAGTGCCTGCGATCCCTCTGTGTCCATGGGGCCCTG
  CACATAACCCTCAGCTTCACCTACATGAACAGCATGCTGGATCCCCTGGTGTATTATTTT
  781 CACATAACCCTCAGCTTCACCTACATGAACAGCATGCTGGATCCCCTGGTGTATTATTTT
   TICCAGCIGGAGIICITIAIGCCCCICGGCAICAICITAITITGCICCTICAAGAIIGII
  TGGAGCCTGAGGCGAGCCAGCAGCTGGCCAGACAGGCTCGGATGAAGAAGGCGACCCGG
  rheumatoid arthritis; autoimmune disorder; respiratory ailment;
  Human nGPCR11 coding sequence #2.
   BP
   CACATTGTTGAGTGGCACTGA 1041
  1021 CACATTGTTGAGTGGCACTGA 1041
   AAH51008 standard; DNA; 1041
   16-NOV-2000; 2000WO-US31581
   (first entry)
   neuroprotective;
   28-AUG-2001
   AAH51008
   1021
  Homo
   181
   541
  781
  961
          421
  421
   481
  601
   661
   721
  AAH51008
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   hRUP19 The endogenous and non-endogenous, constitutively activated versions of human G-protein coupled receptors (GPCR), are useful for direct identification of candidate compounds as receptor agonists, inverse agonists or partial agonists having applicability as therapeutic agents for treating diseases related to GPCR, e.g. lung cancer. Mon-endogenous version of human GPCRs are also utilized in research settings and in vitro and in vivo system, incorporating GPCRs can be utilized to elucidate and understand the roles these receptors play in the human condition, both normal and diseased.
  Endogenous and non-endogenous versions of human G-protein coupled receptors for direct identification of candidate compounds as agonists, inverse agonists or partial agonists for use as therapeutic agents -
  240
   120
  180
  180
   300
   300
  360
  360
   420
   CTGCTCATTGTGGCCTTTGTGCTGGCGCGCACTAGGCGATGGGGTCGCCCTGTGTGGTTTC 120
  9
   9
  Gaps
  CACCACGCGGTGAACACTATCTCCACCCGGGTGGCGGCTGGCATCGTGTGCACCCTGTGG
  CTGCTCATTGTGGCCCTTTGTGCTGGGCGCACTAGGCAATGGGGTCGCCCCTGTGTGGTTTC
  TGCTTCCACATGAAGACCTGGAAGCCCAGCACTGTTTACCTTTTCAATTTGGCCGTGGCT
   GGGACCATCGTGTTCCTTACGGTGGTGGCTGCGGACAGGTATTCAAAGTGGTCCACCC
  ATGTACAACGGGTCGTGCTGCCGCATCGAGGGGGACACCATCTCCCAGGTGATGCCGCCG
   ATGTACAACGGGTGCTGCCGCATCGAGGGGGACACCATCTCCCCAGGTGATGCCGCCG
  GATTTCCTCCTTATGATCTGCCTGCCTTTTCGGACAGACTATTACCTCAGACGTAGACAC
   TGGGCTTTTTGGGGACATTCCCTGCCGAGTGGGGCTCTTCACGTTGGCCATGAACAGGGCC
  GGGAGCATCGTGTTCCTTACGGTGGTGGCTGCGGACAGGTATTTCAAAGTGGTCCACCCC
  100.0%; Score 1041; DB 22; Length 1041; 100.0%; Pred. No. 4e-288; 0; Indels 0; Mismatches 0; Indels 0;
   sequence encodes a human G-protein coupled receptor (GPCR)
   Sequence 1041 BP; 208 A; 294 C; 278 G; 261 T; 0 other;
  Claim 47; Page 110; 159pp; English
14-MAR-2000; 2000US-0189258.
14-MAR-2000; 2000US-0189259.
10-APR-2000; 2000US-0195898.
10-APR-2000; 2000US-0195899.
10-APR-2000; 2000US-0196078.
12-MAY-2000; 2000US-0200419.
12-JUN-2000; 2000US-0210982.
  Dang HT, Lowitz KP;
   Best Local Similarity 100.0%;
Matches 1041; Conservative (
  (AREN-) ARENA PHARM INC
  2001-355616/37
   P-PSDB; AAU04373
  Match
  Chen R,
   61
  121
  121
  181
   241
  301
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  361
   361
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9 600 720 720 780 780 840 900 900 960

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Human; GCPR; G-coupled protein-receptor; cardiant; antiarteriosclerotic; anabolic; cytostatic; antiviral; gene therapy; cardiomyopathy; obesity; annorexia; diabetes; osteoporosis; Crohn's disease; multiple sclerosis; asthma; Alzheimer's disease; Parkinson's disease; Huntington's disease; infection; human immunodeficiency virus; HIV; ds.
   961 AGGAGTTGCATCAGTGTGGCAAATAGTTTCCAAAGCCAGTCTGATGGGCAATGGGATCCC 1020
   CAGCCAGGACACTCAAAAACACAAAAGGCCGGAAGAGAGATGCCAATTTCGAACCTCGGTCGC
  CACCACGCGGTGAACACTATCTCCACCCGGGTGGCGCTGGCATGGTTGTCTGCACCCTGTGG
  TTCATCATGGTGGTGGCAATTGTGTTCATCACATGCTACCTGCCCAGCGTGTCTGCTAGA
  CTCTATTTCCTCTGGACGGTGCCTCGAGTGCCTGCGATCCCTCTGTCCATGGGGCCCTG
   CACATAACCCTCAGCTTCACCTACATGAACAGCATGCTGGATCCCCTGGTGTATTATTTT
              TGGGCTTTTGGGGACATTCCCTGCCGAGTGGGGCTCTTCACGTTGGCCATGAACAGGGCC
                               GCCCTGGTCATCCTGGGAACAGTGTATCTTTTGCTGGAGAACCATCTCTGCGTGCAAGAG
   TICCAGCIGGAGIICTITATGCCCCTCGGCATCATCTTATITTGCTCCTTCAAGAITGTT
  TGGAGCCTGAGGCGGAGGCAGCTGGCCAGACAGGCTCGGATGAAGAAGGCGACCCGG
  CTCTATTTCCTCTGGACGGTGCCCTCGAGTGCCTGCGATCCCTCTGTCCATGGGGCCCTG
   CACATAACCCTCAGCTTCACCTACATGAACAGCATGCTGGATCCCCTGGTGTATTATTTT
  TCAAGCCCCTCCTTTCCCAAATTCTACAACAAGCTCAAAATCTGCAGTCTGAAACCCAAG
   CAGCCAGGACACTCAAAAACACAAAGGCCGGAAGAGATGCCAATTTCGAACCTCGGTCGC
   GGGAGCATCGTGTTCCTTACGGTGGTGGCTGCGGACAGGTATTTCAAAGTGGTCCACCCC
   SEQ ID
   BP
  1021 CACATTGTTGAGTGGCACTGA 1041
  ABA81529 standard; DNA; 1050
  polynucleotide
   (first entry)
   Human GPCRla
   28-JAN-2002
  ABA81529
  481
   901
   1021
               241
   301
   301
  361
  361
  421
   421
   481
   541
  601
  601
  661
   661
  721
  721
   781
   781
   901
   RESULT 4
ABA81529
  g
   qq
  Q
  g
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  g
   q
   δ
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  g
  ò
   g
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   The present invention relates to novel G protein-coupled receptors

(nGPCRx; where x is 1, 3, 4, 5, 9, 11, 12, 14-18, 20, 21, 22, 24, 27,

28, 31-38, 40, 41, 53-60) and their coding sequences. The present

sequence is the coding sequence for one such G protein-coupled receptor.

GPCRs are also known as seven transmembrane receptors and function in

signal transduction. The nGPCRx coding sequences are useful for

screening a human to diagnose a disorder affecting the brain or a genetic

c predisposition, specifically schizophrenia. nGPCRx are useful for

cneptRx in a sample is useful for treating schizophrenia. Detection of

cneptRx in a sample is useful for treating schizophrenia. Detection of

clasorders infections such as HIV-1, metabolic and cardiovascular

clasorders, infections such as HIV-1, metabolic and cardiovascular

clasorace; proliferative disorders and hormonal disorders. Modulators of

nGPCRx activity have the utility for treating neurological disorders,

clasorace; proliferative disorder), and neuronal disorders such as

clasorace; apprintment of disorder), and neuronal disorders such as

clasorace; rheumatoid arthritis, autoimmune disorders, cancers,

conditional disorders include inflammatory conditions (e.g. Crohn's

crespiratory aliments auch as asthma, and inflammatory diseases e.g.
   ö
   CTGCTCATTGTGGCCTTTGTGCTGGCGCACTAGGCAATGGGGTCGCCCTGTGTGGTTTC 120
  TGCTTCCACATGAAGACCTGGAAGCCCAGCACTGTTACCTTTTCAATTTGGCCGTGGCT 180
   Gaps
  New G protein-coupled receptor (nGPCR-x) and its encoding polynucleotide useful for diagnosing and treating e.g. schizophrenia
  1 ATGTACAACGGGTCGTGCTGCCGCATCGAGGGGGACACCATCTCCCAGGTGATGCCGCCG 60
  9
  Slightom J;
tz T, Huff
  TGCTTCCACATGAAGACCTGGAAGCCCAGCACTGTTTACCTTTTCAATTTGGCCGTGGCT
  GATTTCCTCCTTATGATCTGCCTGCCTTTTCGGACAGACTATTACCTCAGACGTAGACAC
   Lind P, Slight
V, Sejlitz T,
  Sequence 1041 BP; 208 A; 294 C; 278 G; 261 T; 0 other;
  PS, Bannigan CM, Ruff
   Hiebsch RR,
  Claim 4; Page 89; 261pp; English
   Parodi LA,
   (PHAA ) PHARMACIA & UPJOHN CO
  20000S-0186811.
20000S-0188114.
20000S-0198110.
20000S-0198568.
20000S-0198568.
           990S-0166071.
990S-0166678.
990S-0173396.
2000US-0185421.
2000US-018554.
2000US-0185554.
   08-MAY-2000; 2000US-0203111.
   inflammatory bowel disease.
   Best Local Similarity 100. Matches 1041; Conservative
  Kaytes
   WPI; 2001-389826/41,
   Wood LS,
   P-PSDB; AAG80968
   21-MAR-2000;
20-APR-2000;
02-MAY-2000;
   22-FEB-2000;
28-FEB-2000;
28-FEB-2000;
02-MAR-2000;
  Schellin KA,
  03-MAR-2000;
09-MAR-2000;
17-MAR-2000;
   ο̈
  Query Match
  Vogeli
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   121
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Length 1050

100.0%;

Similarity

Query Match

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CURA-) CURAGEN CORP.
   WPI; 2001-639351/73.
  P-PSDB; ABB44522
        WO200174904-A2.
                                  06-APR-2000; 2
06-APR-2000; 2
06-APR-2000; 2
06-APR-2000; 2
06-APR-2000; 2
   27-JUL-2000;
28-JUL-2000;
   sapiens
                                06-APR-2000;
   06-APR-2000;
   21-JUL-2000;
  29-MAR-2001;
              11-0CT-2001
  «ajumder K,
  Padigaru M,
  Ношо
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New human G-protein coupled receptor X, GPCRX, polypeptide useful in treatment or prevention of GPCRX associated disorders e.g. cardiomyopathy or atherosclerosis, and to screen for antagonists and agonists useful therapeutically SK; Spaderna S Li L; ŗ, Wolenc AR, Spytek KA, Vernet CAM, Casman SJ, Mishnu VS, Tchernev VT, 11-AUG-2000; 2000US-224588P. 11-CCT-2000; 2000US-236513P. 18-JAN-2001; 2001US-262508P. 23-JAN-2001; 2001US-263604P. 23-JAN-2001; 2001US-263604P. 30-JAN-2001; 2001US-265161P. 2000US-219855P. 2000US-221284P. 2000US-221325P. 2000US-195068P. 2000US-195069P. 2000US-195070P. 2000US-195066P. 2000US-195067P. 2001US-265161P 2001US-0823172 30-MAR-2001; 2001WO-US10241 2000US-195510P Baumgartner JC, Gusev VY;

The invention relates to nucleic acid sequences (ABAB1529-ABAB152) that encode G-coupled protein-receptor related polypeptides

(ABB44527-ABB44543). The isolated polypeptide having a sequence differing by no more than 15 % of amino acid residues from one of 22 amino acid captures forms of the sequences), fully defined in the sequences (or mature forms of the sequences), fully defined in the specification and corresponding to human G-protein coupled receptor X (GPCRX) polypeptides. The polypeptides have potential cardiant, antiarteriosclerotic, anabolic, cytostatic and antiviral activity. The polypeptides can be administered therapeutically, especially using gene polypeptides can be administered therapeutically, especially using gene compared to stand an expressing and mercoding DNA in vivo, to treat or prevent GPCRX-associated disorders, especially in humans. For example, they can be used to treat/prevent cardiomyopathy, atherosclerosis, disorders compession and metabolic pathway modulation (e.g. disease, multiple solesity, anorexia), diabetes, osteoporosis, crohn's disease, multiple calerosis, asthma, cancers, neurodegenerative disorders (e.g. Alzheimer's diseases, Parkinson's disorder, Huntington's disease, immune disorders, hadmatopoietic disorders, developmental diseases, immune disorders, conferently, fungal, protozoal and viral infections (e.g. with humans) by detecting alterations in polypeptide expression levels relative to control samples. They are useful to identify agents binding polypeptide control samples they are useful to identify agents binding polypeptide control and equivation or activity, useful as modulating callular polypeptide expression or activity, useful as modulating callular polypeptide expression or activity, useful as Claim 9; Page 7; 157pp; English

996 961 ò a Sequence 1050 BP; 211 A; 299 C; 279 G; 261 T; 0 other;

AGGAGTTGCATCAGTGTGGCAAATAGTTTCCAAAGCCAGTCTGATGGGCAATGGGATCCC 1020 240 300 305 360 365 420 425 480 485 540 900 605 099 999 720 7.25 780 785 840 845 120 125 Gaps 9 65 126 TGCTTCCACATGAAGACCTGGAAGCCCAGCACTGTTTACCTTTTCAATTTGGCCGTGGCT GGGAGCATCGTGTTCCTTACGGTGGTGGTGCTGCGGACAGGTATTTCAAAGTGGTCCACCCC 66 CTGCTCATTGTGGCCTTTGTGCTGGGCGACTAGGCAATGGGGTCGCCTGTGTGGTTTC 186 GATTTCCTCCTTATGATCTGCCTGCCTTTTCGGACAGACTATTACCTCAGACGTAGACAC GCCCTGGTCATCCTGGGAACAGTGTATCTTTTGCTGGAGAACCATCTCTGCGTGCAAGAG TGGAGCCTGAGGCGGAGCCAGCAGCTGGCCAGGCTCGGATGAAGAAGGCGACCCGG TTCATCATGGTGGTGCCAATTGTGTTTCATCACATGCTACCTGCCCAGCGTGTCTGCTAGA CTCTATTTCCTCTGGACGGTGCCCTCGAGTGCCTGCGATCCCTCTGTCCATGGGGCCCTG 1 ATGTACAACGGGTCGTGCTGCCGCATCGAGGGGGACACCATCTCCCAGGTGATGCCGCCG 121 IGCTICCACAIGAAGACCIGGAAGCCCAGCACIGITIACCITITCAAITIGGCCGIGGCT GATITICCICCITAIGAICIGCCIGCCITITICGGACAGACTAITACCICAGACGIAGACAC 301 GGGAGCATCGTGTTCCTTACGGTGGTGGCTGCGGACAGGTATTTCAAAGTGGTCCACCCC 361 CACCACGCGGTGAACACTATCTCCCACCCGGGTGGCGGCTGGCATCGTCTGCACCTGTGG GCCCTGGTCATCCTGGGAACAGTGTATCTTTTGCTGGAGAACCATCTCTGCGTGCAAGAG CACATAACCCTCAGCTTCACCTACATGAACAGCATGCTGGATCCCCTGGTGTATTATTTT TCAAGCCCCTCCTTTCCCAAATTCTACAACACCTCAAAATCTGCAGTCTGAAACCCAAG CAGCCAGGACACTCAAAAACACAAAGGCCGGAAGAGATGCCCAATTTCGAACCTCGGTCGC TGGGCTTTTGGGGGCACATTCCCTGCCGAGTGGGGCTCTTCACGTTGGCCATGAACAGGGCC TGGAGCCTGAGGCGGAGGCAGCTGGCCAGACAGGCTCGGATGAAGAAGGCGACCCGG ö Indels ; Score 1041; DB 2; Pred. No. 4e-288; 0; Mismatches 0 Conservative Best Local Sim Matches 1041; 9 306 366 126 486 909 984 846 906 241 121 481 601 991 999 721 726 781 841 901 8 õ 셤 ð 셤 δ q ò qq ò g ò Ор ò g ò g ò g ò g ò g à 셤 ò 셤 ò 셤 ò g

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can be administered therapeutically, especially using gene
   TTCATCATGGTGGTGGCAATTGTGTTCATCACATGCTACCTGCCCAGCGTGTCTGCTAGA 725
  Matches 1041; Conservative
   Similarity
 polypeptides
   Query Match
  Best Local
   246
  99
   121
  126
  181
   186
   241
   301
   306
  366
  421
  126
  486
  541
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   The invention relates to nucleic acid sequences (ABA81529-ABA81552) that encode G-coupled protein-receptor related polypeptides (ABB44543). The isolated polypeptide having a sequence differing by no more than 15 % of amino acid residues from one of 22 amino acid sequences (or mature forms of the sequences), fully defined in the sequences (or mature forms of the sequences), fully defined in the sequences) polypeptides. The polypeptides have potential cardiant, antiarteriosclerotic, anabolic, cytostatic and antiviral activity. The
   anabolic; cytostatic; antiviral; gene therapy; cardiomyopathy; obesity; anorexia; diabotes; osteoporosis; Crohn's disease; multiple sclerosis; asthma; Alzheimer's disease; Parkinson's disorder; Huntington's disease; infection; human immunodeficiency virus; HIV; ds.
  GCPR; G-coupled protein-receptor; cardiant; antiarteriosclerotic;
   New human G-protein coupled receptor X, GPCRX, polypeptide useful in treatment or prevention of GPCRX associated disorders e.g. cardiomyopathy or atherosclerosis, and to screen for antagonists and agonists useful therapeutically
  Spaderna SK;
Li L;
  Wolenc AR,
Spytek KA,
  Human GPCR1b polynucleotide SEQ ID NO 3.
  Vernet CAM, Casman SJ,
Mishnu VS, Tchernev VT,
   Claim 9; Page 10; 157pp; English.
            CACATTGTTGAGTGGCACTGA 1046
   ABA81530 standard; DNA; 1050 BP
1021 CACATTGTTGAGTGGCACTGA 1041
   2000US-195066P.
2000US-195067P.
2000US-195068P.
  2000US-221284P.
2000US-221325P.
2000US-224588P.
   2000US-194614P.
2000US-195063P.
   2001US-262508P.
   2001US-263433P.
2001US-263604P.
   30-MAR-2001; 2001WO-US10241
   2000US-195069P
  2000US-195070P
  2000US-195510P
  2000US-219855P
   2000US-239613P
  2001US-265161P
   2001US-0823172
  Gusev VY:
  28-JAN-2002 (first entry)
   (CURA-) CURAGEN CORP.
   2001-639351/73.
  Baumgartner JC,
  P-PSDB; ABB44522
  WO200174904-A2
   06-APR-2000;
06-APR-2000;
06-APR-2000;
06-APR-2000;
06-APR-2000;
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  18-JAN-2001;
   23-JAN-2001;
  31-MAR-2000;
   27-JUL-2000;
28-JUL-2000;
   29-MAR-2001;
   05-APR-2000;
06-APR-2000;
  06-APR-2000;
  21-JUL-2000;
  11-AUG-2000;
  11-OCT-2000;
  23-JAN-2001;
  30-JAN-2001;
  Majumder K,
Padigaru M,
   11-0CT-2001
  ABA81530;
                     1026
   ABA81530
  RESULT
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CPCRX associated disorders, especially in humans. For example, they can be used to treat/prevent cardiomyopathy, atherosclerosis, disorders related to signal processing and metabolic pathway modulation (e.g. obesity, anorexia), diabetes, osteoporosis, Crohn's disease, multiple sclerosis, asthma, cancers, neurodegenerative disorders (e.g. Alzheimer's disease, Parkinson's disorders, developmental disease), immune disorders, hematopoletic disorders, developmental diseases, neurological disorders, bacterial, fungal, protozoal and viral infections (e.g. with human conferency virus (HIV)-1 or HIV-2). They can be used dispnostically to detecrine the presence of or predisposition to a disease associated with altered levels of the polypeptide expression levels relative to control samples. They are useful to dentify agents binding polypeptide control samples. They are useful dentify agents binding polypeptide control samples of or propertied expression or activity, useful as
  480
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  240
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  720
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   365
  425
  485
   605
  61 CTGCTCATTGTGGCCCTTTGTGCTGGCCGCACTAGGCAATGGGGTCGCCCTGTGTGTTTC 120
   9
   65
  Gaps
   GATTTCCTCCTTATGATCTGCCTGCCTTTTCGGACAGACTATTACCTCAGACGATAGACAC
   GCCCTGGTCATCCTGGGAACAGTGTATCTTTTGCTGAGAACCATCTCTGTGCGAGAAGA
   TGGAGCTGAGGCGGAGGAGCAGCAGCAGCCAGACAGGCTCGGATGAAGAAGGAGCACCCGG
  TTCATCATGGTGGTGGCAATTGTGTTCATCACATGCTACCTGCCCAGCGTGTCTGCTAGA
   1 ATGTACAACGGGTCGTGCTGCCGCATCGAGGGGGACACCATCTCCCCAGGTGATGCCGCCG
   TGCTTCCACATGAAGACCTGGAAGCCCAGCACTGTTTACCTTTTCAATTTGGCCGTGGCT
  GATTTCCTCCTTATGATCTGCCTGCCTTTTTCGGACAGACTATTACCTCAGACGTAGACAC
  361 CACCAGGGGGTGAACACTATCTCCACCGGGTGGCGGCTGGCATCGTCTGCACCCTGTGG
   TICCAGCTGGAGTTCTTTATGCCCCTCGGCATCATCTTATTTTGCTCCTTCAAGATTGTT
  TGGAGCCTGAGGCGGAGCCAGCAGCTGGCCAGGCTCGGATGAAGAAGGCGACCCGG
  TGGGCTTTTTGGGGGACATTCCCTGCCGAGTGGGGGCTCTTCACGTTGGCCATGAACAGGGCC
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   100.0%; Score 1041; DB 22; Length 1050; 100.0%; Pred. No. 4e-288; Live 0; Mismatches 0; Indels 0;
  Sequence 1050 BP; 211 A; 298 C; 279 G; 262 T; 0 other;
  antagonists and agonists in disease treatment.
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Query Match
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  ò
   셤
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  961 AGGAGTTGCATCAGTGTGGCAAATACTTTCCAAAGCCAGTCTGATGGGCAATGGGATCCC 1020
   966 AGGAGTTGCATCAGTGTGGCAAATAGTTTCCAAAGCCAGTCTGATGGGCAATGGGATCCC 1025
   arteriosclerosis; hepatitis; cancer; neurological disorder; epilepsy; Alzhahaer's disease; parkinson's disease; cardiovascular disorder; atherosclerosis; hypertension; myocardial infarction; peptic ulcer; gastrointestinal disorder; dysphagia; anorexia; autoimmune disorder; acquired immune deficiency syndrome; inflammatory disorder; infection; Addison's disease; allergy; Grave's disease; metabolic disorder; AlDS; diabetes; obesity; osteoporosis; gene therapy; GCREC-3; ss.
                                   840
  900
   905
  CAGCCAGGACACTCAAAAACACAAAGGCCGGAAGAGATGCCAATTTCGAACCTCGGTCGC 960
         845
   965
   Graul R;
721 CTCTATTTCCTCTGGACGGTGCCCTCGAGTGCCTGCGATCCCTCTGTCCATGGGGCCCTG
  841 TCAAGCCCCTCCTTTCCCAAATTCTACAAGATCTCAAAAATCTGCAGTCTGAAACCCCAAG
   Hafalia A;
Au-Young J;
                                  781 CACATAACCCTCAGCTTCACCTACATGAACAGCATGCTGGATCCCCTGGTGTATTTTT
   Human; G-protein coupled receptor 3; cell proliferative disorder;
  /product= "Human mature GCREC-3 protein"
   , Thornton M, Lu Y, Tribouley Walia NK, Nguyen DB, Yue H, Reddy R, Kallick DA, Tang TY,
  Human G-protein coupled receptor 3 (GCREC-3) cDNA.
  /*tag= a
/product= "Human GCREC-3 protein"
|3..138
   Location/Qualifiers
  AAD26371 standard; cDNA; 1083 BP
   1026 CACATTGTTGAGTGGCACTGA 1046
   CACATTGTTGAGTGGCACTGA 1041
  2000US-205628P.
2000US-206222P.
2000US-207566P.
  2000US-208861P.
  (INCY-) INCYTE GENOMICS INC.
  17-MAY-2001; 2001WO-US16285
   2000US-208834P
  (first entry)
   /*tag- b
   /*tag=
  DAM,
  AR,
P,
  Patterson C, Lu
Khan FA, Gandhi
   Lal
   40200187937-A2
  02-JUN-2000;
02-JUN-2000;
   Khan FA, Gan
Elliott VS,
  Homo sapiens
  18-MAY-2000;
22-MAY-2000;
   25-MAY-2000;
   26-MAR-2002
  sig_peptide
  22-NOV-2001
  mat_peptide
  AAD26371;
  901
  1021
  AAD2637
   RESULT
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The invention relates to numen o'protein coupled receptor (Geraco)

To invention relates to numen o'protein coupled receptor (Geraco)

Screening compounds that modulate their activity. They are useful in

the dagnosis, prevention and treatment of disorders which include

cell proliferative disorders such as epilepsy, ischaemic

myelofibrosis, psoriasis and cancer including adenocarcinoma, leukaemia,

Iymphoma; neurological disorders such as epilepsy, ischaemic

crebrovascular disease, Alzheimer's disease, Pick's disease, dementia,

Parkinson's disease, ataxias, multiple sclerosis, bacterial and viral

meningitis, Creutfeldt-Jakob disease, schizophrenic disorders, annesia;

cardiovascular disorders such as arterlovemous fistula, atherosclerosis,

hypertension, vascular tumours, myocardial infarction, hypertensive

cardiovascular disorders such as dysphagial peptic oesophagitis,

meningitis, contestinal disorders such as dysphagial peptic oesophagitis,

cardiovascular disorders such as dysphagial peptic oesophagitis,

emesis, anorexia, nausea, peptic ulcer, cholelithiasis, diarrhoca,

constipation, acquired immune deficiency syndrome (AIDS), hepatic

constipation, acquired immune deficiency syndrome (AIDS), hepatic

constipation, acquired immune deficiency syndrome (AIDS), hepatic

constipation, systemic lupus erythematosus, and trauma;

disease, allergies, spondylitis, amyloidosis, anaemia, asthma, contact

cumpal, parasitic, protozoal and helminthic infections and trauma;

metabolic disorders such as diabetes, obesity and osteoporosis; and

viral infections such as diabetes, obesity and osteoporosis; and

curral infections such as diabetes, obesity and osteoporosis; and

viral infections such as diabetes, obesity and osteoporosis; and

care useful as probes for assessing toxicity of test compounds. They
  Novel G-protein coupled receptors and polynucleotides useful for diagnosis, treatment and prevention of disorders of cell proliferation, neurological, cardiovascular, metabolic disorders and viral infections
   240
   162
  222
   282
   300
   342
  360
  61 CTGCTCATTGTGGCCTTTGTGCTGGGCGCACTAGGCAATGGGGTCGCCCTGTGTGGTTTC 120
  402
  420
   403 CACCACGGGTGAACACTATCTCCACCGGGTGGCGGCTGGCATCGTCTGCACCTGTGG 462
  9
   also used in gene therapy. The present sequence is human G-protein coupled receptor 3 (GCREC-3) CDNA.
  1 ATGTACAACGGGTCGTGCTGCCGCATCGAGGGGGACACCATCTCCCAGGTGATGCCGCCG
   103 CTGCTCATTGTGGCCTTTGTGCTGGGCGCACTAGGCAATGGGGTCGCCCTGTGTGGTTTC
  121 TGCTTCCACATGAAGACCTGGAAGCCCAGCACTGTTTACCTTTTCAATTTGGCCGTGGCT
   181 GATTTCCTCCTTATGATCTGCCTGCCTTTTCGGACAGACTATTACCTCAGACGTAGACAC
  241 TGGGCTTTTGGGGACATTCCCTGCCGAGTGGGGCTCTTCACGTTGGCCATGAACAGGGCC
   GGGAGCATCGTGTTCCTTACGGTGGTGGCTGCGGACAGGTATTTCAAAGTGGTCCACCCC
   CACCACGCGGTGAACACTATCTCCACCCGGGTGGCGGCTGGCATCGTCTGCACCCTGTGG
  The invention relates to human G-protein coupled receptor (GCREC)
  100.0%; Score 1041; DB 24; Length 1083; 100.0%; Pred. No. 4.1e-288;
  ö
  Indels
  Sequence 1083 BP; 211 A; 314 C; 288 G; 270 T; 0 other;
  0; Mismatches
  Claim 5; Page 112; 115pp; English.
   Best_Local Similarity 100. Matches 1041; Conservative
WPI; 2002-089844/12.
P-PSDB; AAE16172.
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  protozoacide; analgesic; cytostatic; neuroleptic; nootropic; anticonvulsant; tranquilliser; viral infection; pain; cancer; anorexia; bulimia; asthma; central nervous system disease; CNS disease; cardiovascular disease; hypotension; hypertension; angina pectoris; myocardial infarction; urinary retention; osteoporosis; ulcer; asthma; inflammation; altergy; benign prostatic hypertrophy; multiple sclerosis; psychotic disorder; neurological disorder; dyskinesia; huntington's disease; Touretter's syndrome; anxiety; schizophrenia; manic depression; delirium; dementia; mental retardation; ss.
  961 AGGAGTTGCATCAGTGTGGCAAATAGTTTCCAAAGCCAGTCTGATGGGCAATGGGATCCC 1020
  702
  720
  762
  780
  822
   900
   HM74-like GPCR; G-protein coupled receptor; antibacterial; fungicide;
   TCAAGCCCCTCCTTCCCAAATTCTACAACAAGCTCAAAATCTGCAGTCTGAAACCCCAAG
  GCCCTGGTCATCCTGGGAACAGTGTATCTTTTGCTGGAGAACCATCTCTGCGTGCAAGAG
   CTCTATTTCCTCTGGACGGTGCCCTCGAGTGCCTGCGATCCCTCTGTCCATGGGGCCCTG
   TCAAGCCCCTCCTTTCCCAAATTCTACAACACCTCAAAATCTGCAGTCTGAAACCCAAG
   CAGCCAGGACACTCAAAAACACAAAGGCCGGAAGAGATGCCAATTTCGAACCTCGGTCGC
  TTCCAGCTGGAGTTCTTTATGCCCCTCGGCATCATCTTATTTTGCTCCTTCAAGATTGTT
  TGGAGCCTGAGGCGGAGCAGCAGCTGGCCAGGCTCGGATGAAGAAGGCGGACCCGG
  TTCATCATGGTGGTGGCAATTGTGTTCATCACATGCTACCTGCCCAGCGTGTCTGCTAGA
  CACATAACCCTCAGCTTCACCTACATGAACAGCATGCTGGATCCCCTGGTGTATTATTTT
   cDNA encoding HM74-like G-protein coupled receptor (GPCR).
  /*tag= a
/product= "HM74-like_GPCR"
  Location/Qualifiers
464..1504
  BP
  CACATTGTTGAGTGGCACTGA 1041
  AAS18501 standard; cDNA; 1730
  26-FEB-2002 (first entry)
  /*tag=
  sapiens
  AAS18501;
   1063
  Ношо
  523
  643
   1003
  463
  541
  583
  601
  661
  703
  721
  763
   823
   841
   883
   943
   1021
  181
  781
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human HM74-like G-protein coupled receptor (GPCR) polypeptide. Reagents
that regulate HM74-like GPCR are useful for modulating the activity of
that regulate HM74-like GPCR are useful for modulating the activity of
the protein in a disease selected from bacterial, fungal, protozoan, and
the protein in a disease selected from bacterial, fungal, protozoan, and
consists of system (CNS) disease, cardiovascular disease, hypotension, hypotension,
angina pectoris, myocardial infarction, urinary retention, osteoporosis,
candina pectoris, myocardial infarction, urinary retention, osteoporosis,
ulcer, asthma, inflammation, allergy, benign prostatic hypotension,
candina pectoris and dyskinesia such as Huntington's disease and
rourette's syndrome. The composition is also useful for treating
constructed and neurological disorders such as anxiety, schizophrenia,
manic depression, delirium, dementia and severe mental retardation. (I)
con the HM74-like GPCR polypeptide are also useful for treating the above
cor the HM74-like GPCR polypeptide are also useful for treating the above
cor the HM74-like GPCR described in the method of the invention of polyclonal antibodies. This sequence and munise a mammal
cor provide therapeutic effects. The polypeptide is also useful as a balt
cor provide therapeutic effects. The polypeptide is also useful as a balt
cor provide therapeutic effects. The polypeptide is also useful as a balt
cor provide therapeutic effects. The polypeptide is also useful as a mammal
cor production of polyclonal antibodies. This sequence encodes the human
   Novel isolated polynucleotide, useful for treating infection, pain, cancer, asthma, hypertension, myocardial infarction, urinary retention, osteoporosis, encodes the human HM74-like G-protein coupled receptor polypeptide
  120
  180
   703
  763
   9
   TGGGCTTTTGGGGACATTCCCTGCCGAGTGGGGCTCTTCACGTTGGCCATGAACAGGGCC
   1 ATGTACAACGGGTCGTGCTGCCGCATCGAGGGGGACACCATCTCCCAGGTGATGCCGCCG
  CTGCTCATTGTGGCCTTTGTGCTGGGCGCACTAGGCAATGGGGTCGCCTGTGTGTTTC
   TGCTTCCACATGAAGACCTGGAAGCCCAGCACTGTTTACCTTTTCAATTTGGCCGTGGCT
   GATTTCCTCCTTATGATCTGCCTGCCTTTTCGGACAGACTATTACCTCAGACGTAGACAC
  100.0%; Score 1041; DB 24; Length 1730; 100.0%; Pred. No. 5.1e-288; tive 0; Mismatches 0; Indels 0;
   Sequence 1730 BP; 361 A; 494 C; 444 G; 431 T; 0 other;
/note= "G-protein coupled receptor"
   Claim 1; Fig 1; 77pp; English
  2000US-194701P
   04-APR-2001; 2001WO-EP03811
  Conservative
  WPI; 2002-049147/06.
   Similarity
   (FARB ) BAYER AG
   P-PSDB; AAU11401
  WO200177320-A2.
  05-APR-2000;
   18-OCT-2001
   Best Local Sim
Matches 1041;
   Query Match
   Kiao Y;
  61
   121
   181
  644
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  Human, G-protein coupled receptor; GPCR; chemokine receptor; protease;
hyperproliferative disorder; neurological disorder; psychiatric disease;
inflammatory disorder; respiratory disorder; gene therapy; ds.
  AGGAGTIGCATCAGTGTGGCAAATAGTTTCCAAAGCCAGTCTGATGGGCAATGGGATCCC 1020
   1004 TTCCAGCTGGAGTTCTTTATGCCCCTCGGCATCTTATTTTGCTCCTTCAAGATTGTT 1063
  1423
   720
  099
  840
  960
             823
                          420
  540
   900
  CTCTATTTCCTCTGGACGGTGCCCTCGAGTGCCTGCGATCCCTCTGTCCATGGGGCCCTG 780
                                       883
   GCCCTGGTCATCCTGGGAACAGTGTATCTTTTGCTGGAGAACCATCTCTGCGTGCAAGAG 480
  CACATAACCCTCAGCTTCACCTACATGAACAGCATGCTGGATCCCCTGGTGTATTTTT
   CAGCCAGGACACTCAAAAACACAAAAGGCCGGAAGAGATGCCAAATTTCGAACCTCGGTCGC
  TTCATCATGGTGGTGGCAATTGTGTTCATCACATGCTACCTGCCCAGCGTGTCTGCTAGA
GGGAGCATCGTGTTCCTTACGGTGGTGGCTGCGGACAGGTATTTCAAAGTGGTCCACCCC
       CACCACGCGGTGAACACTATCTCCACCGGGTGGCGGCTGGCATCGTCTGCACCCTGTGG
   TGGAGCCTGAGGCGGAGGCAGCAGCTGGCCAGACAGGCTCGGATGAAGAAGGCGACCCGG
   Gene encoding novel human G protein-coupled receptor (GPCR).
   вр
  CACATTGTTGAGTGGCACTGA 1041
   1484 CACATTGTTGAGTGGCACTGA 1504
   DNA; 2331
   (first entry)
  AAS12582 standard;
   WO200173029-A2
   Homo saptens
   19-DEC-2001
   04-OCT-2001
  AAS12582;
301
  721
  1424
                          361
   421
   481
  661
  901
  196
  601
  781
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The present invention relates to the isolation of a novel human G-protein coupled receptor (GPCR) which is related to the chemokine receptor subfamily. The CDNA and gene sequences encoding for GPCR are also given in the invention. The sequences of the invention are useful for diagnosing and treating diseases or conditions mediated by human proteases. Such diseases include hyperproliferative disorders (e.g. hyperplasia), neurological disorders (e.g. Parkinson's disease), psychiatric diseases (e.g. schizophrenia), inflammatory disorders (e.g. diabetes) and respiratory disorders (e.g. diabetes) and respiratory disorders (e.g. also useful for identifying a modulator of the expression of the protein is also useful for identifying agents for use in mammalian therapeutic applications, e.g. a human drug, particularly modulating a blological or pathological response in a cell or tissue that expresses the protein, in biological creeptor subfamily, in drug screening assays and in competition binding assays and screening assays and in competition binding assays. GPCR is also useful in diagnosing a disease or predisposition to polynocleotide sequences can also be used in gene thersent
   molecules encoding the protein for use in developing human therapeutics and diagnostic compositions and for identifying modulators of the
  490
  610
   360
  Gaps
  9
  1 ATGTACAACGGGTCGTGCTGCCGCATCGAGGGGGACACCATCTCCCCAGGTGATGCCGCCG
   61 CIGCICATIGIGGCCITIGIGCIGGCGCACIAGGCAAIGGGGICGCCCIGIGIGITIC
  181 GATTTCCTCCTTATGATCTGCCTGCCTTTTTCGGACAGACTATTACCTCAGACGTAGACAC
  121 TGCTTCCACATGAAGACCTGGAAGCCCAGCACTGTTTACCTTTTCAATTTGGCCGTGGCT
  GGGACCATCGTGTTCCTTACGGTGGTGGTGCGACAGGTATTCAAAGTGGTCCACCCC
   611 GGGAGCATCGTGTTCCTTACGGTGGTGGCTGCGGACAGGTATTTCAAAGTGGTCCACCCC
   sequence represents the human GPCR gene sequence of the invention
  CACCACGCGGTGAACACTATCTCCACCCGGGTGGCGGCTGGCATCGTCTGCACCCTGTGG
   human G-protein coupled receptor proteins and nucleic acid
   Query Match 100.0%; Score 1041; DB 22; Length 2331; Best Local Similarity 100.0%; Pred. No. 5.9e-288; Matches 1041; Conservative 0; Mismatches 0; Indels 0;
   Sequence 2331 BP; 497 A; 620 C; 592 G; 622 T; 0 other;
   Ë
   Beasley
   Francesco V,
  Claim 23; Fig 3; 66pp; English.
  2000US-192419P.
2000US-230459P.
2000US-0666535.
27-MAR-2001; 2001WO-US09522
   ρį
   WPI; 2001-616503/71.
   Cravchik A,
   (PEKE ) PE CORP NY
  27-MAR-2000;
06-SEP-2000;
  20-SEP-2000;
  protein
   Ye J,
   Novel
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Human; GCPR; G-coupled protein-receptor; cardiant; antiarteriosclerotic; anabolic; cytostatic; antiviral; gene therapy; cardiomyopathy; obesity; anorexala; diabetes; osteoporosis; Crohn's disease; multiple sclerosis; asthma; Alzhelmer's disease; Parkinson's disorder; Huntington's disease; infection; human immunodeficiency virus; HIV; ds.
   1030
   1090
  1150
   TCAAGCCCCTCCTTTCCCAAATTCTACAACAAGCTCAAAATCTGCAGTCTGAAACCCAAG 1210
   TTCATCATGGTGGTGGCAATTGTGTTCATCACATGCTACCTGCCCAGCGTGTCTGCTAGA 720
   CTCTATTTCCTCTGGACGTGCCCTCGAGTGCCTGCGATCCCTCTGTCCATGGGGCCCTG 780
                               GCCCTGGTCATCCTGGGAACAGTGTATCTTTTGCTGGAGAACCATCTCTGCGTGCAAGAG 790
  TCAAGCCCCTCCTTTCCCAAATTCTACAAGAGCTCAAAATCTGCAGTCTGAAAGCCCAAG
          GCCCTGGTCATCCTGGGAACAGTGTATCTTTTGCTGGAGAACCATCTCTGCGTGCAAGAG
  TTCCAGCTGGAGTTCTTTATGCCCCTCGGCATCATCTTATTTTGCTCCTTCAAGATTGTT
  CACATAACCCTCAGCTTCACCTACATGAACAGCATGCTGGATCCCCTGGTGTATTTTT
   AGGAGTTGCATCAGTGTGGCAAATAGTTTCCAAAGCCAGTCTGATGGGCAATGGGATCCC
  TTCCAGCTGGAGTTCTTTATGCCCCTCGGCATCATCTTATTTTGCTCCTTCAAGATTGTT
  TGGAGCCTGAGGCGGAGCCAGCAGCTGGCCAGGCTCGGATGAAGAAGGCGACCCGG
  CAGCCAGGACACTCAAAAACACAAAAGGCCGGAAGAGATGCCAATTTCGAACCTCGGTCGC
   Human GPCR1c polynucleotide SEQ ID NO 4.
   1331 CACATTGTTGAGTGGCACTGA 1351
  CACATTGTTGAGTGGCACTGA 1041
  ABA81531 standard; DNA; 1104 BP
   (first entry)
  28-JAN-2002
   Homo sapiens
   . ABA81531;
   1211
   1031
  1001
  1151
   1021
                               731
   191
   541
   851
  601
   661
  971
  721
  781
  841
  961
   1271
           121
  481
  901
   ABA8153.
  RESULT
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The invention relates to nucleic acid sequences (ABAB1529-ABAB152) that encode G-coupled protein-receptor related polypeptides

CG (ABB44522-ABB4443). The isolated polypeptides

CG (ABB44522-ABB4443). The isolated polypeptides

CG (ABB44522-ABB4443). The isolated polypeptides having a sequence differing

CG (ABB44522-ABB4443). The isolated polypeptide having a sequence differing

CG (ABB44522-ABB4443). The isolated polypeptides from one of 22 amino acid

CG (ABB44522-ABB4443). The isolated polypeptides from one of 22 amino acid

CG (GPCRX) polypeptides. The polypeptides have potential cardiant.

CG (GPCRX) polypeptides. The polypeptides have potential cardiant.

CG (GPCRX) polypeptides can be administered therapeutically, especially, using gene

CG can be used to treat or prevent

CG (GPCRX-associated disorders, especially in humans. For example, they can

CG be used to treat/prevent cardiomyopathy, atherosclerosis, disorders

CC celerosis, astima, cancers, neurodegenerative disorders,

CG be used to treat/prevent cardiomyopathy, atherosclerosis, disorders,

CG be used to treations's disorder, Huntington's disease, multiple

CC controllarial, fungal, protozoal and viral infections (e.g. with human

CC mamunodeficiency virus (HV)-1 or predisposition to a disease associated

CC control samples. They are useful to identify agents binding polypeptide

CC collular receptors or downstream effectors) and/or agents

CC modinaliaring cellular polypeptide expression levels relative to

CC modinaliaring cellular polypeptide expression activity, typerial
  CTGCTCATTGTGGCCTTTGTGCTGGGCGCACTAGGCAATGGGGTCGCCCTGTGTGGTTTC 120
  9
  New human G-protein coupled receptor X, GPCRX, polypeptide useful in treatment or prevention of GPCRX associated disorders e.g. cardlomyopathy or atherosclerosis, and to screen for antagonists and
   Gaps
  1 ATGTACAACGGGTCGTGCTGCCGCATCGAGGGGGACACCATCTCCCCAGGTGATGCCGCCG
  modulating cellular polypeptide expression or activity, useful as antagonists and agonists in disease treatment.
   DB 22; Length 1104;
  SK;
   Spaderna :
L1 L;
   2; Indels
   Sequence 1104 BP; 216 A; 318 C; 295 G; 275 T; 0 other;
  Wolenc AR,
Spytek KA,
   Pred. No. 3.4e-287;
0; Mismatches 2;
   99.7%; Score 1037.8;
   Vernet CAM, Casman SJ,
Mishnu VS, Tchernev VT,
   Claim 9; Page 11; 157pp; English.
  agonists useful therapeutically
06-APR-2000; 2000US-195066P.
06-APR-2000; 2000US-195067P.
06-APR-2000; 2000US-195068P.
06-APR-2000; 2000US-195070P.
06-APR-2000; 2000US-19510P.
21-JUL-2000; 2000US-219510P.
27-JUL-2000; 2000US-21284P.
28-JUL-2000; 2000US-224588P.
11-AGG-2000; 2000US-224588P.
11-AGG-2000; 2000US-224588P.
11-AGG-2000; 2000US-224588P.
11-AGG-2000; 2000US-224588P.
11-AGG-2000; 200UUS-265508P.
23-JAN-2001; 2001US-265508P.
23-JAN-2001; 2001US-265508P.
23-JAN-2001; 2001US-265508P.
23-JAN-2001; 2001US-265161P.
29-MAR-2001; 2001US-265161P.
   99.88;
   Baumgartner JC, Gusev VY;
   Matches 1039; Conservative
  (CURA-) CURAGEN CORP.
   WPI; 2001-639351/73.
   Local Similarity
  P-PSDB; ABB44523
  Majumder K,
Padigaru M,
   Query Match
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2000US-193664P. 2000US-194614P. 2000US-195063P.

31-MAR-2000; 05-APR-2000; 06-APR-2000;

30-MAR-2001; 2001WO-US10241

WO200174904-A2.

11-0CT-2001

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1079
  1019
  1020
   539
  540
  780
   840
  959
   960
  180
                    239
  240
   299
   300
  359
  360
  419
  420
  479
  480
  599
  900
   629
   099
   719
  TTCATCATGGTGGTGCAATTGTGTTCATCACATGCTACCTGCCCAGCGTGTCTGCTAGA 720
  779
  839
   899
  900
360 GGGAGCATCGTGTTCCTTACGGTGGTGGCTGCGGCAGGTATTTCAAAGTGGTCCCCC
   TGGGCTTTTGGGGACATTCCCTGCCGAGTGGGGCTCTTCACGTTGGCCATGAACAGGGCC
   TGGCCTTTTGGGGACATTCCCTGCCGAGTGGGGCTCTTCACGTTGGCCATGAACAGGGCC
   GCCCTGGTCATCCTGGGAACAGTGTATCTTTTGCTGGAGAACCATCTCTGCGTGCAAGAG
  CTCTATTTCCTCTGGACGGTGCCCTCGAGTGCCTGCGATCCCTCTGTCCATGGGGCCCCTG
   TCAAGCCCCTCCTTTCCCAAATTCTACAAGAGCTCAAAATCTGCAGTCTGAAACCCAAG
   961 AGGAGTTGCATCAGTGTGGCAAATAGTTTCCAAAGCCAGTCTGATGGGCAATGGGATCCC
  1020 AGGAGTTGCATCAGTGTGGCAAATAGTTTCCAAAGCCAGTCTGATGGGCAATGGGATCCC
   240 GATTTCTCTCTTATGATCTGCCTGCCTTTTCGGACAGACTATTACCTCAGACGACAGACTACACA
   CACCACGCGGTGAACACTATCTCCACCGGGTGGCGGCTGGCATCGTCTGCACCCTGTGG
  TGGAGCCTGAGGCGGAGCAGCTGGCCAGACAGGCTCGGATGAAGAAGGCGACCCGG
   840 CACATAACCCTCAGCTTCACCTACATGAACAGCATGCTGGATCCCCTGGTGTATTTTT
   901 CAGCCAGGACACTCAAAAACACAAAAGGCCGGAAGAGATGCCAATTTCGAACCTCGGTCGC
                                       GATITICCTCCTTATGATCTGCCTGCCTTTTCGGACAGACTATTACCTCAGACGTAGACAC
   GGGAGCATCGTGTCCTTACGGTGGTGCTGCGGACAGGTATTTCAAAGTGGTCCACCCC
   CACATAACCCTCAGCTTCACCTACATGAACAGCATGCTGGATCCCCTGGTGTATTTTT
  1080 CACATTGTTGAGTGGCACTGA 1100
   1021 CACATTGTTGAGTGGCACTGA 1041
                   180
   241
   300
  301
   420
  421
   540
   720
  780
   781
   841
   006
                                       181
   361
   481
   601
  661
  721
121
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signal transduction; nGPCR; seven transmembrane receptor; signal transduction; schizophrenia; thyroid disorder; renal fallure; rheumatoid arthritis; CNS disorder; infection; metabolic disease; cardiovascular disease; proliferative disorder; hormonal disorder; neurological disorder; neuronal disorder; Alzheimer's disease; cancer; attention deficit-hyperactivity disorder/attention deficit disorder; Parkinson's disease; migraine; senile dementia; inflammatory disease; rheumatoid arthritis; autoimmune disorder; respiratory ailment; neuroprotective; ds.
       coding sequence #1.
  (PHAA ) PHARMACIA & UPJOHN CO
  2000US-0185421.
2000US-0185554.
2000US-0186530.
   2000US-0188114.
2000US-0190310.
   99US-0166678
99US-0173396
  2000US-0190800
  2000US-0198568
2000US-0201190
  2000US-0184129
   2000US-0186811
   2000WO-US31581
  2000US-0203111
  20000S-0207094
  WO200136473-A2
       nGPCR11
  03-MAR-2000;
09-MAR-2000;
17-MAR-2000;
21-MAR-2000;
20-APY-2000;
08-MAY-2000;
   17-NOV-1999;
19-NOV-1999;
28-DEC-1999;
22-FEB-2000;
  28-FEB-2000;
28-FEB-2000;
02-MAR-2000;
   Homo sapiens
  16-NOV-2000;
   25-MAY-2000;
   25-MAY-2001
        Human
```

Hiebsch RR, Lind P, Slightom J; an CM, Ruff V, Sejlitz T, Huff Bannigan CM, Parodi LA, PS, Bannie Kaytes WPI; 2001-389826/41. P-PSDB; AAG80934 KA, Schellin

Wood LS,

Vogeli G,

₹,

Claim 4; Page 77; 261pp; English.

New G protein-coupled receptor (nGPCR-x) and its encoding polynucleotide useful for diagnosing and treating e.g. schizophrenia

The present invention retarces to novel to protein couplete incuples. The present invention retarces to novel to protein couplete incuples. 24, 27, 28, 31-38, 40, 41, 53-60) and their coding sequences. The present consists are also known as seven transmembrane receptors and function in captured in the coding sequence and function in captured in the coding sequence are useful for captured in a sequence and function in captured in a predisposition. The nGPCRx coding sequences are useful for captured in a predisposition, specifically schizophrenia nGPCRx are useful for deanness a disorder affecting the brain or a genetic conformation of nGPCRx in a sample is useful as a diagnostic tool for diseases or disorders, infections such as HIV-1, metabolic and cardiovascular disorders, infections such as HIV-1, metabolic and cardiovascular diseases, proliferative disorders and hormonal disorders. Modulators of cofPCRx activity have the utility for treating neurological disorders, including schizophrenia, ADHD/ADD (attention deficit disorder), and neuronal disorders such as include inflammatory conditions (e.g. Crohn's disease), rheumatolid arthritis, autolymmune disorders, cancers, concers, co present invention relates to novel G protein-coupled receptors

inflammatory bowel disease.

BP.

AAH50974 standard; DNA; 888

RESULT 1

AAH50974;

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28-AUG-2001 (first entry)

us-09-886-041-1.std.rng

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(first entry)
  WPI; 1999-095273/08.
  P-PSDB; AAW94654
29-APR-1999
   Homo sapiens
  WO9856820-A1
   12-JUN-1998;
  12-JUN-1997;
  allergies
  17-DEC-1998
   Query Match
  Bergsma
   Matches
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  300
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   TGCTTCCACATGAAGACCTGGAAGCCCAGCACTGTTTACCTTTTCAATTTGGCCGTGGCT 180
   GATTTCCTCCTTATGATCTGCCTGCCTTTTCGGACAGACTATTACCTCAGACGTAGACAC 240
  300
   CACCACGCGGTGAACACTATCTCCACCCGGGTGGCGGCTGGCATCGTCTGCACCCTGTGG 420
   900
  TTCATCATGGTGGTGGCAATTGTGTTCATCACATGCTACCTGCCCAGCGTGTCTGCTAGA 720
   999
  840
  61 CTGCTCATTGTGGCCTTTGTGCTGGGCGCACTAGGCAATGGGGTCGCCCTGTGTGGTTTC 120
                                Gaps
  GCCCTGGTCATCCTGGGAACAGTGTATCTTTGCTGGAGAACCATCTCTGCGTGCAAGAG
   CACATAACCCTCAGCTTCACCTACATGAACAGCATGCTGGATCCCCTGGTGTATTTTT
  TCAAGCCCTCTTTCCCAAATTCTACAACAAGCTCAAAATCTGCAGTCTGAAAGCCCAAG
  TGGGCTTTTGGGGACATTCCCTGCCGAGTGGGGCTCTTCACGTTGGCCATGAACAGGGCC
   TGGAGCCTGAGGCGGAGGCAGCTGGCCAGACAGGCTCGGATGAAGAAGGCGACCCGG
  CACATAACCCTCAGCTTCACCTACATGAACAGCATGCTGGATCCCCTGGTGTATTTTT
  TCAAGCCCCTCCTTTCCCAAATTCTACAACAAGCTCAAAATCTGCAGTCTGAAACCCAAG
                               ö
   948
                              Indels
                Length
   CAGCCAGGACACTCAAAAACACAAAGGCCGGAAGAGATGCCAATTTCG
Sequence 888 BP; 174 A; 254 C; 231 G; 229 T; 0 other;
              85.3%; Score 888; DB 22; L
100.0%; Pred. No. 2.7e-244;
ive 0; Mismatches 0;
                              Matches 888; Conservative
                       Similarity
              Query Match
                        Local
  RESULT 11
AAX16671
   Н
   121
  181
   181
   121
  241
  241
  301
   421
  361
   481
  421
   541
   181
  601
  541
  661
   601
  721
  661
   721
   781
  901
   841
   301
   361
  781
   841
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The present sequence encodes a member of the G-protein coupled receptor (7TM receptor) family, designated the HM/4A receptor. The proteins, agonists, antagonists and polynucleotides can be used for treating disorders associated with increased or reduced expression or activity of HM/4A, e.g. bacterial, fungal, protozoan and viral infections, particularly infections caused by HIV-1 or HIV-2, pain, cancers, clabetes, obesity, anorexia, bulimia, asthma, Parkinson's disease, acute heart failure, hypotension, hypertension, urinary retention, osteoporosis, angina pectoris, myocardial infarction, stroke, ulcers, asthma, allergies, benign prostatic hypertrophy, migraine, vomiting, psychotic and neurological disorders, including anxiety, schizophrenia manic depression, depression, delitium, dementia, and severe mental retardation, and dyskinesias such as Huntington's disease or cetardation, and dyskinesias such as Huntington's disease or cetardation, and dyskinesias such as Huntington's disease or cetardation.
  HM74A receptor; G-protein coupled receptor; infection; pain; cancer; diabetes; obesity; neurological disorder; heart failure; hypertension; asthma; allergy; ss.
   240
   180
   97 ATAGACAAGAACTGCTGTGTTCCGAGATGACTTCATTGTCAAGGTGTTGCCGCCG 156
   Gaps
  New isolated G-protein coupled receptor, HM74A - used to develop products for treating e.g. infections, pain, cancers, diabetes, obesity, neurological disorders, heart failure, hypertension, asthma
  GATTTCCTCCTTATGATCTGCCTGCCTTTTCGGACAGACTATTACCTCAGACGTAGACAC
   1 ATGTACAACGGGTCGTGCTGCCGCATCGAGGGGGACACCATCTCCCCAGGTGATGCCGCCG
   CTGCTCATTGTGGCCTTTGTGCTGGGCGCACTAGGCAATGGGGTCGCCTGTGTGGTTTC
   121 TGCTTCCACATGAAGACCTGGAAGCCCAGCACTGTTTACCTTTTCAATTTGGCCGTGGCT
  Length 1361;
   18;
  Mooney JL;
  / Match 35.8%; Score 372.4; DB 20; Length Local Similarity 64.2%; Pred. No. 2.1e-96; les 600; Conservative 0; Mismatches 316; Indels
  Sequence 1361 BP; 291 A; 390 C; 342 G; 338 T; 0 other;
   Li X,
coupled receptor HM74A encoding cDNA.
   DJ, Elshourbagy NA, Guerrera SF,
  "HM74A receptor"
  detection, diagnosis and drug screening.
   Location/Qualifiers
61..1152
   Claim 2; Page 30-31; 40pp; English.
   (SMIK ) SMITHKLINE BEECHAM CORP.
  97US-0049480.
  98WO-US12386
   /*tag= a
/product=
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AAX16671 standard; cDNA; 1361

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AAX16671;

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   882
277 GACTITCTACTGATCATCTGCCTGCCCTTCCTGATGGACAACTATGTGAGGCGTTGGGAC 336
                           396
   360
   456
  GCCCTGGTCATCCTGGGAACAGTGTATCTTTTGCTGGAGAACCATCTCTGCGGTGCAAGAG 480
  753
  934 GIGGIGIACIATITITICCAGCCCATCCTITICCCAACITICITICTACCACTITIGATCAACCGC 993
  397 GGCAGCATCATTCTTCACGGTGGTGGTAGACAGGTATTTCCGGGTGGTCCATCCC
  517 GCCATCACTATTGGCCTGACAGTCCACCTCCTGAAGAAGAAGATGCCGATCCAGAATGGC
  541 TICCAGCIGGAGTICTITATGCCCCTCGGCATCATCTTATTTTGCTCCTTCAAGATTGTT
   TGGAGCCTGAGGCGGAGCAGCTGGCCAGACAGGCTCGGATGAAGAAGAGGCGACCCGG
  721 CTCTATTTCCTCTGGACGGTGCCCTC------GAGTGCCTGCGATCCCTCT
   814 ATCCGCATCTTCTGGCTCCTGCACACTTCGGGCACGCAGAATTGTGAAGTGTACCGCTCG
  826 CTGGTGTATTATTTTCAAGCCCCTCCTTTCCCAAATTCTACAACAAGCTCAAAATCTGC
  CACCACGCGGTGAACACTATCTCCACCGGGTGGCGGCTGGCATCGTCTGCACCCTGTGG
   766 GTCCATGGGGCCCTGCACATAACCCTCAGCTTCACCTACATGAACAGCATGCTGGATCCC
  GGGAGCATCGTGTTCCTTACGGTGGTGGCTGCGGACAGGTATTTCAAAGTGGTCCACCCC
  Human; G-protein coupled receptor; GPCR; hRUP25; agonist;
inverse agonist; lung cancer; ss.
  cDNA encoding G-protein coupled receptor,
   886 AGTCTGAAACCCAAGCAGCAGGACACTCAAAAA 919
  Location/Qualiflers
1..1092
/*tag= a
   /product- "hRUP25"
   AAS07952 standard; cDNA; 1092
   (first entry)
   WO200136471-A2
   Homo sapiens
   23-OCT-2001
   AAS07952;
   Human
   457
  421
   301
  361
   601
  AAS07952
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The sequence encodes a human G-protein coupled receptor (GPCR), hRUP25. The endogenous and non-endogenous, constitutively activated versions of human G-protein coupled receptors (GPCR), are useful for direct identification of candidate compounds as receptor agonists, inverse agonists or partial agonists having applicability as therapeutic agents for treating diseases related to GPCR, e.g. lung cancer. Non-endogenous version of human GPCRs are also utilized in research settings and in vitro and in vivo system, incorporating GPCRs can be utilised to elucidate and understand the roles these receptors
  Endogenous and non-endogenous versions of human G-protein coupled receptors for direct identification of candidate compounds as agonists, inverse agonists or partial agonists for use as therapeutic agents -
  61 CTGCTCATTGTGGCCTTTGTGCTGGCCGCACTAGGCAATGGGGTCGCCCTGTGTGGTTTC 120
   TGCTTCCACATGAAGACCTGGAAGCCCAGCACTGTTTACCTTTTCAATTTGGCCGTGGCT 180
   241 TGGGCTTTTGGGGACATTCCCTGCCGAGTGGGGCTCTTCACGTTGGCCATGAACAGGGCC 300
  Gaps
  1 ATGTACAACGGGTCGTGCTGCCGCATCGAGGGGGACACCCATCTCCCAGGTGATGCCGCCG 60
   181 GATTTCCTCTTATGATCTGCCTGCCTTTTCGGACAGACTATTACCTCAGACGTAGACAC
   DB 22; Length 1092;
   Mismatches 318; Indels
   Sequence 1092 BP; 223 A; 320 C; 273 G; 276 T; 0 other;
   play in the human condition, both normal and diseased
   Score 369.2; DB 2
Pred. No. 1.6e-95;
   Claim 71; Page 120-121; 159pp; English
   ,
0
  9905-0171901
9905-0171902
20000US-01181925
20000US-01189259
20000US-0195899
2000US-0195899
   35.5%;
  99US-0166099.
99US-0166369.
99US-0171900.
   Dang HT, Lowitz KP
   2000US-0242343
  2000WO-US31509
  Conservative
   (AREN-) ARENA PHARM INC
  WPI; 2001-355616/37.
P-PSDB; AAU04379.
   Query Match
Best Local Similarity
Matches 598; Conserv
  23-DEC-1999;
23-DEC-1999;
11-FEB-2000;
  14-MAR-2000;
14-MAR-2000;
10-APR-2000;
10-APR-2000;
  26-SEP-2000;
20-OCT-2000;
  0-APR-2000;
  28-APR-2000;
12-MAY-2000;
  12-JUN-2000;
  2-JUN-2000;
  21-AUG-2000;
26-SEP-2000;
16-NOV-2000;
   23-DEC-1999;
  Chen R,
  37
  121
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us-09-886-041-1.std.rng

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CACCACGCGGTGAACACTATCTCCCACCCGGGTGGCGGCTGGCATCGTCTGCACCCTGTGG 420
   900
  99
   765
  CTGGTGTATTATTTTCAAGCCCCTCCTTTCCCAAATTCTACAACAAGCTCAAAATCTGC 885
   GTGGTGTACTACTACTACCAGCCCATCCTTTCCCAACTTCTTCTCCACTTTGATCAACCGC 933
  754 Arccecarcricrescrecrecacarresses 813
  GCCCTGGTCATCCTGGGAACAGTGTATCTTTTGCTGGAGAACCATCTCTGCGTGCAAGAG
   TGGAGCCTGAGGCGGAGGCAGCTGGCCAGACAGGCTCGGATGAAGAAGGCGACCCGG
   CACCAGGCCCTGAACAAGATCTCCAATCGGACAGCAGCCATCATCTTGTGTGG
   GGTGCAAATTTGTGCAGCAGCTTCAGCATCTGCCATACCTTCCAGTGGCACGAAGCCATG
   TTCCAGCTGGAGTTCTTTATGCCCCTCGGCATCATCTTATTTTGCTCCTTCAAGATTGTT
   CTCTATTTCCTCTGGACGGTGCCCTC------GAGTGCCTGCGATCCCTCT
   GTCCATGGGGCCCTGCACATAACCCTCAGCTTCACCTACATGAACAGCATGCTGGATCCC
                              GGGAGCATCGTGCTTACGGTGGTGGTGCGGACAGGTATTTCAAAGTGGTCCACCCC
   G protein-coupled receptor; GPCR; constitutively active; intracellular loop 3; transmembrane domain 6; drug screening; agonist; antagonist; ss.
   886 AGTCTGAAACCCAAGCAGCCAGGACACTCAAAAA 919
   Human G protein-coupled receptor HM74 cDNA
   ВР
  AAA30658 standard; cDNA; 1164
  99WO-US23938
   98US-0170496
   (first entry)
  (AREN-) ARENA PHARM INC.
   WO200022129-A1.
  21-AUG-2000
   Homo saptens
   12-OCT-1999;
   13-OCT-1998;
  20-APR-2000
   AAA30658;
         277
                              301
   361
  397
  421
   457
  517
  577
  991
   814
  826
   337
   541
   601
  637
  661
  694
   721
  AAA30658
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The invention relates to constitutively active, non-endogenous versions of endogenous human orphan G protein-coupled receptors (GPCRs, AAY90643-AAY90677 and AAY90677 and AAY90677 and AAA30709-A30743 and AAA30779-A30779). The mutant proteins of the invention contain a mutation in a portion of the protein comprising intracellular loop 3 (IC3) and transmembrane domain 6 (TM6). A non-endogenous anno acid, X, is substituted for an endogenous residue in IC3 at a position 16 amino acids N-terminal of an endogenous proline in TM6 to form a sequence X-(AA)15-Pro. The endogenous amino acid is selected from Lys, His, Arg or Ala, and is preferably Lys. When the endogenous residue at this position is Lys, this residue is replaced by His, Arg or preferably Ala. The 15 amino acid stretch between the substituted amino acid and the Promay be endogenous. Anno-endogenous, or a mixture of endogenous and con-endogenous residues. The constitutively active GPCRs are useful for identifying antagonists, agonists and partial agonists for use as pharmaceutical agents. The mutant proteins are also useful for identifying antagonists. The mutant proteins are also useful for settings for elucidating the roles of the receptors in normal and discassed conditions. Antagonists for a particular GPCR are useful for reacting diseases and discreders associated with that receptor. Because the novel mutant GPCRs are constitutively active, they can be used directly for screening of compounds without the need for endogenous in an exemplification of the invention. This was cloned and subjected unstant of the invention.
  ä
  240
   300
   360
   456
  180
   396
   CACCACGCGGTGAACACTATCTCCACCGGGTGGCGGCTGGCATCGTCTGCACCCTGTGG 420
  GCCCTGGTCATCCTGGGAACAGTGTATCTTTTGCTGGAGAACCATCTCTGCGGTGCAAGAG 480
   CTGCTCATTGTGGCCTTTTGTGCTGGCGCCCACTAGGCAATGGGGTCGCCCTGTGTGGTTTC 120
   97 GTGTTGGGGCTGGAGTTTATCTTTGGGCTTCTGGGCAATGGCCTTGCCCTGTGGATTTTC 156
   9
  Non-endogenous constitutively activated human G protein-coupled receptors, useful for identifying agonists for use as pharmaceutical
  Gaps
  157 TGTTTCCACCTCAAGTCCTGGAAATCCAGCCGGATTTTCCTGTTCAACCTGGCAGTAGCT
   TGGGCTTTTTGGGGACATTCCCTGCCGAGTGGGGCTCTTCACGTTGGCCATGAACAGGGCC
   1 ATGTACAACGGGTCGTGCTGCCGCATCGAGGGGGACACCATCTCCCCAGGTGATGCCGCCG
   301 GGGAGCATCGTGTTCCTTACGGTGGTGGCTGCGGACAGGTATTTCAAAGTGGTCCACCCC
  TGCTTCCACATGAAGACCTGGAAGCCCAGCACTGTTTACCTTTTCAATTTGGCCGTGGCT
  GATTTCCTCCTTATGATCTGCCTGCCTTTTCGGACAGACTATTACCTCAGACGTAGACAC
  DB 21; Length 1164;
  18;
  Score 367.6; DB 21; Length
Pred. No. 4.7e-95;
0; Mismatches 319; Indels
  Sequence 1164 BP; 246 A; 337 C; 288 G; 293 T; 0 other;
   English.
                   Liaw CW;
  Query Match 35.3%;
Best Local Similarity 63.9%;
Matches 597; Conservative 0
   Example 1; Page 185; 341pp;
                   Д,
                Chalmers
   WPI; 2000-329165/28
  P-PSDB; AAY90637
                   Behan DP,
  agents
  217
  121
  181
   241
   277
   337
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TGGAGCCTGAGGCGGAGCCAGCAGCTGGCCAGGCTCGGATGAAGAAGGCGACCCGG
   Query Match
  157
   577
  157
   181
   217
  241
  277
  301
   337
  397
  541
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  720
   753
  873
   933
   Non-endogenous constitutively activated human G protein-coupled receptors, useful for identifying agonists for use as pharmaceutical
   DNA encoding human mutant G protein-coupled receptor HM74 (1230K).
                                      517 CCTGCAAATGTGTGCATCAGCTTCAGCATCTGCCATACCTTCCGGTGGCACGAAGCTATG
   TTCCAGCTGGAGTTCTTTATGCCCCTCGGCATCATCTTATTTTGCTCCTTCAAGATTGTT
  TGGAGCCTGAGGCGAGGCAGCAGCTGGCCAGACAGGCTCGGATGAAGAAGGCGACCCGG
   TTCATCATGGTGGTGGCAATTGTGTTCATCATGCTACCTGCCCAGCGTGTCTGCTAGA
  CTCTATTTCCTCTGGACGGTGCCCTC------GAGTGCCTGCGATCCCTCT
  754 ATCCGCATCTTCTGGCTCCTGCACATTCGGGCACGCAGAATTGTGAAGTGTACCGCTCG
  766 GTCCATGGGGCCCTGCACATAACCCTCAGCTTCACCTACATGAACAGCATGCTGGATCCC
   814 GIGGACCIGGCGTICTITATCACTCTCAGCTTCACCTACATGAACAGCATGCTGGACCCC
   826 CTGGTGTATTATTTTCAAGCCCCTCCTTTCCCAAATTCTACAACAAGCTCAAAATCTGC
                       G protein-coupled receptor; GPCR; constitutively active; intracellular loop 3; transmembrane domain 6; drug screening; agonist; antagonist; mutant; ss.
  886 AGTCTGAAACCCAAGCAGCAGGACACTCAAAAA 919
  934 TGCCTCCAGAGGAAGATGACAGGTGAGCCAGATA 967
   Example 2; Page 285-286; 341pp; English.
   Liaw CW;
  BP
  AAA30738 standard; DNA; 1164
   99WO-US23938
   98US-0170496
  (first entry)
  Chalmers DT,
  (AREN-) ARENA PHARM INC.
   WPI; 2000-329165/28.
P-PSDB; AAY90672.
  WO200022129-A1
  21-AUG-2000
   sapiens
  12-OCT-1999;
   13-OCT-1998;
  30-APR-2000
  3ehan DP,
   Synthetic.
  AAA30738;
   agents
                       481
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AAY30677 and AAY30683-Y90687), and to DNA encoling them (AAA30709-A30743) and AAA30775-A30779). The mutant protein coupled receptors (GPCRS, AAY30687), and to DNA encoling them (AAA30709-A30743) and tanament protein comprising intracellular loop 3 (IC3) and transmembrane domain 6 (TM6). A non-endogenous amino acid, X, is substituted for an endogenous residue in IC3 at a position 16 amino acids N-terminal of an endogenous residue in IC3 at a position of amino acids N-terminal of an endogenous proline in TM6 to form a sequence X-(AA)15-Pro. The endogenous amino acid is selected from Lys, His, Arg or Ala, and is preferably Lys. When the endogenous residue at this position is Lys, this residue is replaced by His, Arg or preferably Ala. The 15 amino acid stretch between the substituted amino acid and the Promay be endogenous, non-endogenous, or a mixture of endogenous and manaceutical agents. The mutant proteins are also useful for identifying antagonists, agonists and partial agonists for use as pharmaceutical agents. The mutant proteins are also useful in research settings for elucidating the roles of the receptors in normal and diseased conditions. Antagonists for a particular GPCR are useful for treating diseases and disorders associated with that receptor. Because the novel mutant GPCRs are constitutively acitive, they can be used directly for screening of compounds without the need for endogenous ligands. Sequences AAA30709-AAA30743 and AAA30779 represent DNAs
  2
to constitutively active, non-endogenous versions
  121 TGCTTCCACATGAAGACCTGGAAGCCCAGCACTGTTTACCTTTTCAATTTGGCCGTGGCT 180
  GATTTCCTCCTTATGATCTGCCTGCCTTTTCGGACAGACTATTACCTCAGACGTAGACAC 240
   TGGGCTTTTGGGGACATTCCCTGCCGAGTGGGGCTCTTCACGTTGGCCATGAACAGGGCC 300
   360
  GGCAGCATCATCTTCCTCACGGTGGTGGCGGTAGACAGGTATTTCCGGGTGGTCCATCC 396
   420
   GCCCTGGTCATCCTGGGAACAGTGTATCTTTTGCTGGAGAACCATCTCTGCGTGCAAGAG 480
   TICCICCIGGAGIICCICCIGCCCCIGGGCAICAICCIGITCIGCICAGCCAGAAITAIC 636
  CTGCTCATTGTGGCCTTTGTGCTGGCGCACTAGGCAATGGGGTCGCCCTGTGTGGTTTC 120
   Gaps
   1 ATGTACAACGGGTCGTGCTGCCGCATCGAGGGGGACACCATCTCCCAGGTGATGCCGCCG 60
   37 ATAGACAAGAAGAACTGCTGTGTTCCGAGATGACTTCATTGCCAAGGTGTTGCCGCCG 96
   GGCATCACTGTTGGCCTAACAGTCCACCTCCTGAAGAAGAAGTTGCTGATCCAGAATGGC
   GGGAGCATCGTGTTCCTTACGGTGGTGCTGCGGACAGGTATTTCAAAGTGGTCCACCCC
  CACCACGCGGTGAACACTATCTCCACCGGGTGGCGGCTGGCATCGTCTGCACCCTGTGG
   TTCCAGCTGGAGTTCTTTATGCCCCTCGGCATCATCTTATTTTGCTCCTTCAAGATTGTT
   Score 366; DB 21; Length 1164;
Pred. No. 1.3e-94;
0; Mismatches 320; Indels 18;
   Sequence 1164 BP; 248 A; 335 C; 289 G; 292 T; 0 other;
   encoding the mutant human GPCRs of the invention.
  35.2%;
63.8%;
  Best Local Similarity 63.8
Matches 596; Conservative
   invention relates
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  Consensus sequences are identified from nine rat gene receptors. The receptors are for somatostatin, substance K, substance P, neuromedin K, thyrotropin, HH/CG and others designated mas, mry and rta. Four regions of nucleotide sequence are found to exhibit a degree of conservation significant enough to design degenerate oligo primers for PCR (see AAQ55045-49). Five oligos are designed with 4 - to 64-fold direct degeneracy plus 5%-23% inosines. The oligos are designed to anneal sequences in G protein-linked peptide receptor genes. They are used as six different primer pairs for PCR using rat genomic DNA
   754 ATCCGCATCTTCTGGCTCCTGCACATTCGGGCACGCAGAATTGTGAAGTGTACCGCTCG 813
   874 GIGGIGIACTACTICTCCAGCCCATCCTTTCCCAACTTCTTCTCCACTTTGATCAACCGC 933
TGGAGCCTGCGGCAGAG---ACAAATGGACCGGCATGCCAAGATCAAGAGCCAAAACC 693
                                  TTCATCATGGTGGTGGCAATTGTGTTCATCACATGCTACCTGCCCAGCGTGTCTGCTAGA
  GTGGACCTGGCGTTCTTTATCACTCTCAGGTTCACCTACATGAACAGCATGCTGGACCCC
  CTCTATTTCCTCTGGACGGTGCCCTC------GAGTGCCTGCGATCCCTCT
   CTGGTGTATTATTTTCAAGCCCCTCCTTTCCCAAATTCTACAACAAGCTCAAAATCTGC
   GTCCATGGGGCCCTGCACATAACCCTCAGCTTCACCTACATGAACAGCATGCTGGATCCC
   Isolation and identifying new receptor DNA - pref. G-protein linked receptors, using PCR with new receptor specific primers
   primer; peptide ligand receptor; ss
  Sequence of orphan receptor DNA fragment PCR
   886 AGTCTGAAACCCAAGCAGCACACACACAAAA 919
  /*tag= b
/label- PCR oligo no. 10
   ω
  Pausch MH;
  Location/Qualifiers
1..26
/*tag a
/label= PCR oligo no.
526..545
   BP
  Claim 6; Fig 3; 17pp; English.
   (AMCY ) AMERICAN CYANAMID CO
  Ozenberger BA,
  AAQ55054 standard; DNA; 546
  92US-0915966
  93EP-0108984
  (first entry)
   *tag=
   WPI; 1994-017562/03.
   misc_feature
  misc_feature
  04-JUN-1993;
  Hadcock JR,
  18-JUL-1994
   PCR; oligo;
   19-JAN-1994
  EP578962-A.
  Synthetic
   AAQ55054;
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  721
   994
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size. DNA fragments are cloned and two samples, designated PCR9 and PCR11AAQ55054,055055), are found to contain sequences characteristic of grotein-linked receptors. Each fragment contains a single ORF. There is considerable similarity between rat sometostatin receptor and PCR11, suggesting that PCR11 is a novel sometostatin receptor subtype. Both fragments exhibit not only primary sequence similarity to other receptors but also the hydropathy pattern characteristic of G protein-linked receptors. The novel G protein-linked receptors are possibly of the peptide ligand subclass.
   61 GGACAACTATGTCCAGAACTGGGACTGGGAGGTTCGGGAGCATCCCCTGCCGCGTGATGCT 120
   335
   395
  240
  515
  275
  575
  635
  157 TACCTTTTCAATTTGGCCGTGGCTGA-TTTCCTCCTTATGATCTGCCTGCCTTTTCGGAC 215
   GGCTGGCATCGTCTGCACCCTGTGGGCCCTGGTCATCCTGGGAACAGTGTATCTTTGCT 455
   301 CACGGACATGATGACCCGGAACGGCGATGCAAACCTGTGCAGCATTTTAGCATCTGCTA 360
  GGCTCGGATGAAGAAGGCGACCCGGTTCATCATGGTGGTGGCAATTGTGTTCATCACATG 695
  CGTCAAGATCAAGAGGGCCATCAACTTCATCATGATGGTGCTTGTGTTTTGCCATCTG 537
  Gaps
template. All six reactions produce DNA fragments of the expected
  1 TTCGTGGTGAACCTGGTCGGGGCTGACTTTTCTCTGATCATTTGCCTTGCCGTTCTTGAC 60
   456 GGAGAACCATCTCTGCGTGCAAGAGACGCCGTCTCCTGTGAGAGCTTCATGAGAGTC
   216 AGACTATTACCTCAGACGTAGACACTGGGCTTTTGGGGACATTCCCTGCCGAGTGGGGCT
   CTTCACGTTGGCCATGAACAGGGCCGGGAGCATCGTGTTCCTTACGGTGGTGGCTGCGGGA
  336 CAGGTATTTCAAAGTGGTCCACCCCCACCACGCGGTGAACACTATCTCCACCCGGGTGGC
   CTTATTTTGCTCCTTCAAGATTGTTTGGAGCCTGAGGCGGAGGCAGCAGCTGGCCAGACA
  GGCCAATGGCTGGCATGACATCATGTTCCAGCTGGAGTTCTTTATGCCCCTCGGCATCAT
  4
   DB 15; Length 546;
   Score 220.2; DB 15; Length
Pred. No. 5.9e-53;
0; Mismatches 188; Indels
   Sequence 546 BP; 106 A; 157 C; 144 G; 139 T; 0 other;
   Query Match 21.2%;
Best Local Similarity 65.0%;
Matches 357; Conservative
   II IIIII
CTGGCTGCC 546
   CTACCTGCC 704
   276
   478
   396
  276
  636
   969
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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October 29, 2002, 03:44:28; Search time 61 Seconds (without alignments) 630.025 Million cell updates/sec Run on:

US-09-886-041-2 1853 1 MYNGSCCRIEGDTISQVMPP......ANSFQSQSDGQWDPHIVEWH 346

Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

747574 segs, 111073796 residues Searched: Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

•• Database

A\_Geneseq\_032802

1. /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:\*
2. /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:\*
3. /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:\*
4. /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:\*
5. /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:\*
5. /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:\*
6. /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:\*
7. /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:\*
8. /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:\*
9. /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:\*
110. /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:\*
121. /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1990.DAT:\*
122. /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:\*
123. /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:\*
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155. /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:\*
165. /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:\*
176. /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:\*
177. /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:\*
187. /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:\*
188. /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:\*
199. /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:\*
190. /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:\*
191. /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:\*
192. /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:\*
203. /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:\*
217. /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:\*
218. /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:\*
229. /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

|   | Description              | Human GPCR1a polyp | Novel human G prot | Human G-protein co | Human nGPCR11 #2. | Human GPCR1c polyp | Human nGPCR11 #1. | G-protein coupled | Human G-protein co | Human mutant G pro | Human G protein-co | Human CON103 G pro |
|---|--------------------------|--------------------|--------------------|--------------------|-------------------|--------------------|-------------------|-------------------|--------------------|--------------------|--------------------|--------------------|
|   | ID                       | 1                  | AAU06197           | AAU04373           | AAG80968          | ABB44523           | AAG80934          | AAW94654          | AAU04379           | AAY90672           | AAY90637           | AAE02493           |
|   | DB                       | 22                 | 22                 | 22                 | 22                | 22                 | 22                | 20                | 22                 | 21                 | 21                 | 22                 |
|   | Query<br>Match Length DB | 346                | 346                | 346                | 346               | 346                | 296               | 363               | 363                | 387                | 387                | 384                |
| Ф | Query<br>Match           | 100.0              | 100.0              | 100.0              | 100.0             | 99.5               | 84.7              | 47.7              | 47.7               | 47.6               | 47.5               | 28.5               |
|   | Score                    | 1853               | 1853               | 1853               | 1853              | 1839               | 1570              | 883.5             | 883.5              | 881.5              | 880.5              | 529                |
|   | Result<br>No.            | 1                  | α                  | ٣                  | 4                 | 'n                 | ø                 | 7                 | 8                  | 6                  | 10                 | 11                 |

| Human 7-transmembr | Human opioid-type | Human G-protein co | Human cell surface | Human 7-transmembr | Human G-protein co | Human G protein-co | Human mutant G pro | Human G-protein co | Human G-protein co | Human G-protein co | Human P2Y-like GPC | Human G-protein co | Human G-protein co | Human G-protein co | Cysteinyl leukotri | Human LTC4 recepto | Pig LTC4 receptor | Human G-protein co | Truncated cysLT2 c | Human cysLT2 cyste | Rat cysLT-like rec | Rat LTC4 receptor | Human P2-purinergi | Human 7-transmembr | Seven transmembran | Human G-protein th | Human R12 seven tr | Human 7TM receptor | Human G protein-co | Human P2Y-like GPC | Human mutant G pro | Human G protein co | Human receptor-ass |
|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| ō                  | AAG78785          | 9                  | 33                 | AAW88461           | AAY79157           | AAY90625           | AAY90659           | AAM52651           | AAE07539           | AAE12022           | AAB82852           | AAE07538           | AAU04368           | AAU04383           | AAU07294           | AAB73097           | AAB73098          | AAE08553           | AAB85097           | AAB85094           | AAB85095           | AAB73099          | AAE04389           | AAW62597           | AAR53752           | AAW07617           | AAW48733           | AAB21697           | AAY90618           | AAB82853           | AAY90652           | AAY79576           | AAY69989           |
| 20                 | 22                | 22                 | 21                 | 20                 | 21                 | 21                 | 21                 | 22                 | 22                 | 22                 | 22                 | 22                 | 22                 | 22                 | 22                 | 22                 | 22                | 22                 | 22                 | 22                 | 22                 | 22                | 22                 | 19                 | 15                 | 18                 | 19                 | 21                 | 21                 | 22                 | 21                 | 21                 | 21                 |
| 423                | 423               | 423                | 455                | 476                | 319                | 319                | 319                | 319                | 341                | 346                | 346                | 346                | 346                | 346                | 346                | 346                | 345               | 346                | 331                | 347                | 309                | 309               | 373                | 370                | 339                | 339                | 339                | 339                | 339                | 339                | 339                | 309                | 309                |
| В.                 | 28.5              | ъ.                 | æ                  | ۲.                 | 24.4               | 24.2               | 24.2               | 24.2               | σ.                 | 6                  | σ.                 | σ.                 | σ,                 | σ.                 | ď.                 | ď.                 |                   | 6                  | 19.3               | σ.                 | 6                  | 9                 | σ.                 | 18.7               |                    | 8                  | 8                  | ω.                 | œ                  | 8                  | 18.1               | 7                  | 7                  |
|                    |                   |                    |                    |                    |                    | 48.                | 48.                | 448.5              | 99                 | 66.                | 66.                | . 99               | 99                 | 99                 | . 99               | 66.                | 9                 |                    | 2                  | S                  |                    | 55.               | 2                  |                    | ന                  | m                  | ന                  | m                  | 3                  | 3                  | 3                  | $^{\circ}$         | $\sim$             |
| 12                 | 13                | 14                 | 15                 | 16                 | 17                 | 18                 | 19                 | 20                 | 21                 | 22                 | 23                 | 24                 | 25                 | 26                 | 27                 | 28                 | 29                | 30                 | 31                 | 32                 | 33                 | 34                | 35                 | 36                 | 37                 | 38                 | 39                 | 40                 | 41                 | 42                 | 43                 | 44                 | 45                 |

# ALIGNMENTS

```
Human; GCPR; G-coupled protein-receptor; cardiant; antiarteriosclerotic; anabolic; cytostatic; antiviral; gene therapy; cardiomyopathy; obesity; annoraxia; diabetes; osteoporosis; cronn's disease; multiple sclerosis; asthma; Alzheimer's disease; Parkinson's disorder; Huntington's disease; infection; human immunodeficiency virus; HIV.
  Human GPCRla polypeptide SEQ ID NO 2.
  ABB44522 standard; Protein; 346 AA
   2000US-194614P.
2000US-195063P.
2000US-195066P.
2000US-195067P.
   2000US-195068P.
2000US-195069P.
2000US-195070P.
  30-MAR-2001; 2001WO-US10241
   2000US-195510P
2000US-219855P
  (first entry)
  WO200174904-A2.
   05-APR-2000;
06-APR-2000;
06-APR-2000;
06-APR-2000;
06-APR-2000;
06-APR-2000;
06-APR-2000;
21-JUL-2000;
  Homo sapiens
  31-MAR-2000;
  28-JAN-2002
   11-OCT-2001
   ABB44522;
RESULT 1
ABB44522
   THE STATE OF THE S
```

181 FQLEFFMPLGIILF@SFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSAR 240

```
The invention relates to nucleic acid sequences (ABAB1529-ABAB1552) that encode Groupled protein-receptor related polypeptides as decombled protein-receptor related polypeptides (ABB44522-ABB4443). The isolated polypeptide having a sequence differing by no more than 15 % of amino acid residues from one of 22 amino acid sequences (or mature forms of the sequences), fully defined in the sequences (or mature forms of the sequences), fully defined in the (GPCRX) polypeptides. The polypeptides have potential cardiant, antiarteriosclerotic, anabolic, cytostatic and antiviral activity. The colypeptides can be administered therapeutically, especially using gene therapy and expressing the encoding DNA in vivo, to treat or prevent GPCRX-associated disorders, especially in humans. For example, they can constant processing and metabolic pathway modulation (e.g. cobesity, anorexia), diabetes, osteoporosis, Crohn's disease, multiple cobesity, anorexia), diabetes, osteoporosis, Crohn's disease, multiple cobesity, anorexia, davancers, neurodegenerative disorders, haematopoietic disorders, developmental diseases, neurological disorders, haematopoietic disorders, developmental diseases, neurological disorders, condetermine the presence of or predisposition to a disease associated control samples. They are useful to identify agents binding polypeptide control samples. They are useful to identify agents binding polypeptide control samples. They are useful to identify agents binding polypeptide control samples or benefactors and/or agents
   New human G-protein coupled receptor X, GPCRX, polypeptide useful in treatment or prevention of GPCRX associated disorders e.g. cardiomyopathy or atherosclerosis, and to screen for antagonists and
  modulating cellular polypeptide expression or activity, useful as
antagonists and agonists in disease treatment.
  SK;
  Spaderna S
Li L;
  Wolenc AR,
Spytek KA,
  Casman SJ,
Tchernev VT,
   agonists useful therapeutically
   Claim 1; Page 8; 157pp; English.
                                 2000US-224588P.
2000US-239613P.
2001US-262508P.
2001US-263433P.
2001US-263604P.
2000US-221284P
   2001US-265161P
  29-MAR-2001; 2001US-0823172
  WPI; 2001-639351/73.
N-PSDB; ABA81529, ABA81530.
  Baumgartner JC, Gusev VY;
  Vernet CAM,
   Mishnu VS,
  (CURA-) CURAGEN CORP.
  346 AA;
   23-JAN-2001;
23-JAN-2001;
   30-JAN-2001;
                                      11-AUG-2000;
11-OCT-2000;
  18-JAN-2001;
  Majumder K,
Padigaru M,
   Padigaru
  Sequence
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Sequence
  ö
  61 DFLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHP 120
  HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIM 180
   FQLEFFWPLGIILFCSFKIVWSLRRRQQLARQARWKKATRFIMVVAIVFITCYLPSVSAR 240
  Gaps
   1 MYNGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVA 60
   1 MYNGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVA 60
  ö
100.0%; Score 1853; DB 22; Length 346; 100.0%; Pred. No. 1.2e-199; ive 0; Mismatches 0; Indels 0;
                                      ö
  Matches 346; Conservative
                      Similarity
    Query Match
                        Local
   121
  181
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346 AA

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The present invention relates to the isolation of a novel human G-protein coupled receptor (GPCR) which is related to the chemokine receptor subfamily. The CDNA and gene sequences encoding for GPCR are also given in the invention. The sequences of the invention are useful for diagnosing and treating diseases or conditions mediated by human proteins are also proteases. Such diseases include hyperpoliferative disorders (e.g. hyperplasia), neurological disorders (e.g. parkinson's disease), psychiatric diseases (e.g. schizophrenia), inflammatory disorders (e.g. distress syndrome, ARDS). The GPCR protein is also useful for identifying a modulator of the expression of the protein. It also serves as a target for identifying agents for use in mammallan therapeutic applications, c.g. a human drug particularly modulating a biological or pathological response in a cell or tissue that expresses the protein, in biological cresponse in a cell or tissue that expresses the protein, in biological sasays. GPCR is also useful in diagnosing a disease or predisposition to a disease mediated by the peptide, in pharmacogenomic analysis. The column creamer of the protein generally in the present columns of the invention.
   Human, G-protein coupled receptor; GPCR; chemokine receptor; protease;
hyperproliferative disorder; neurological disorder; psychiatric disease;
inflammatory disorder; respiratory disorder.
   Novel human G-protein coupled receptor proteins and nucleic acid molecules encoding the protein for use in developing human therapeutics and diagnostic compositions and for identifying modulators of the
QPGHSKTQRPEEMPASNLGRRSCISVANSFQSQSDGQMDPHIVEWH 346
   SNLGRRSCISVANSFOSOSDGOWDPHIVEWH 346
  in-coupled receptor (GPCR) protein.
  Beasley EM;
  Di Francesco V,
  Ā
  rotein; 346
   Claim 1; Fig 1; 66pp; English.
  27-MAR-2000; 2000US-192419P.
06-SEP-2000; 2000US-230459P.
20-SEP-2000; 2000US-0666535.
   entry)
   27-MAR-2001; 2001W@-
   OPGHSKTORPEEMP
  Novel human G prote
  AAU06197 standard;
  Ye J, Cravchik A,
   WPI; 2001-616503/7
  N-PSDB; AAS12581
  (PEKE ) PE CORP
  WO200173029-A2
   Homo sapiens.
  04-OCT-2001.
   19-DEC-2001
   AAU06197;
  protein
   301
  301
   RESULT 2
   AAU06197
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(AREN-) ARENA PHARM INC.

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  240
  HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIM 180
   LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK 300
   Gaps
  9
   1 MYNGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVA 60
  MYNGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVA
  181 FQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSAR
                    ö
  Length 346;
   Human; G-protein coupled receptor; GPCR; hRUP19; agonist;
                     Indels
  QPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDPHIVEWH 346
Match
Local Similarity 100.0%; Score 1853; DB 22;
Local Similarity 100.0%; Pred. No. 1.2e-199;
Les 346; Conservative 0; Mismatches 0;
  Human G-protein coupled receptor, hRUP19.
  Ź
  AAU04373 standard; Protein; 346
  20000S-0195899.
20000S-0196078.
20000S-0206119.
20000S-0210741.
20000S-0225760.
20000S-0225779.
20000S-0235779.
20000S-0235418.
20000S-0235418.
   99US-0166088.
99US-0166369.
99US-0171900.
99US-0171901.
99US-0171901.
2000US-0181749.
2000US-0181749.
2000US-0189258.
2000US-0189259.
   Inverse agonist; lung cancer
  16-NOV-2000; 2000WO-US31509
   (first entry)
   WO200136471-A2.
  23-DEC-1999;
23-DEC-1999;
23-DEC-1999;
   14-MAR-2000;
10-APR-2000;
  10-APR-2000;
  10-APR-2000;
28-APR-2000;
   12-JUN-2000;
   26-SEP-2000;
26-SEP-2000;
  23-OCT-2001
   Homo sapiens
   11-FEB-2000;
  14-MAR-2000;
   12-MAY-2000;
   20-OCT-2000;
20-OCT-2000;
  25-MAY-2001.
  17-NOV-1999
   AAU04373;
  Query Match
Best Local 9
                   Matches
   121
   241
   241
  301
   301
  121
  RESULT 3
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   The sequence represents a human G-protein coupled receptor (GPCR), hRUP19. The endogenous and non-endogenous, constitutively activated versions of human G-protein coupled receptors (GPCR), are useful for direct identification of candidate compounds as receptor agonists, inverse agonists or partial agonists having applicability as therapeutic agents for treating diseases related to GPCR, e.g. lung cancer. Non-endogenous version of human GPCRs are also utilized in research settings and in vitro and in vivo system, incorporating GPCRs can be utilised to elucidate and understand the roles these receptors play in the human condition, both normal and diseased.
   receptors for direct identification of candidate compounds as agonists, inverse agonists or partial agonists for use as therapeutic agents -
  G protein-coupled receptor; nGPCR; seven transmembrane receptor; signal transduction; schizophrenia; thyvoid disorder; renal failure; rheumatoid arthritis; CNS disorder; infection; metabolic disease; cardiovascular disease; proliferative disorder; hormonal disorder; neurological disorder; neuronal disorder; Alzheimer's disease; cancer; attention deficit.hyperactivity disorder/attention deficit disorder; Parkinson's disease; migraine; senile dementia; inflammatory disease; rheumatoid arthritis; autoimmune disorder; respiratory ailment;
  DFLLMICLPFRIDYYLRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHP 120
  LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK 300
   Gaps
  1 MYNGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVA 60
   1 MYNGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWRPSTVYLFNLAVA
   181 FQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARWKKATRFIMVVAIVFITCYLPSVSAR
  Endogenous and non-endogenous versions of human G-protein coupled
   .;
0
  100.0%; Score 1853; DB 22; Length 346; 100.0%; Pred. No. 1.2e-199; ive 0; Mismatches 0; Indels 0;
  301 QPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDPHIVEWH 346
   301 QPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGWDPHIVEWH 346
  Claim 45; Page 110-111; 160pp; English.
  ¥.
  AAG80968 standard; Protein; 346
                                  Lowitz KP;
  (first entry)
   Conservative
   WPI; 2001-355616/37
N-PSDB; AAS07946.
  Best Local Similarity
Matches 346; Conserv
                                  Dang HT,
   346 AA;
   Human nGPCR11 #2.
  28-AUG-2001
   AAG80968;
   Sequence
  Query Match
                                  Chen R,
   241
  61
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FOLEFFMPLGIILFCSFKIVWSLRRRQOLARQARMKKATRFIMVVAIVFITCYLPSVSAR

HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIM

QPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDPHIVEWH 346 

A

(first entry)

LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK

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```
61 DFLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHP 120
   Human GPCR1c polypeptide SEQ ID NO 5.
   ABB44523 standard; Protein; 346
  28-JAN-2002
  ABB44523;
  121
   301
                        121
  181
  241
   241
  301
  ABB44523
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   The present invention relates to novel G protein-coupled receptors

(nGPCRx; where x is 1, 3, 4, 5, 9, 11, 12, 14-18, 20, 21, 22, 24, 27,

20, 31-38, 40, 41, 53-60) and their coding sequences. The present

sequence is one such G protein-coupled receptor; GPCRs are also known as

c seven transmembrane receptors and function in signal transduction. The

nGPCRx coding sequences are useful for screening a human to diagnose a

disorder affecting the brain or a genetic predisposition, specifically

c chizophrenia. nGPCRx are useful for identifying compounds useful for

treating schizophrenia. Detection of nGPCRx in a sample is useful as a

diagnostic tool for diseases or disorders e.g. thyroid disorders, renal

fallure, rheumatoid arthritis, CNS disorders, infections such as HIV-1,

metabolic and cardiovascular diseases, proliferative disorders and

c reating neurological disorders, including schizophrenia, ADHD/ADD

c treating neurological disorders, including schizophrenia, ADHD/ADD

c (attention deficit hyperactivity disordery attention deficit disorder),

and neuronal disorders such as Alzheimer's disease, Parkinson's disease,

migraine and senile dementia. Additional disorders include inflammatory

conditions (e.g. Crohn's disease), rheumatoid arthritis, autoimmune

diseases e.g. inflammatory bowel disease.
  Parodi LA, Hiebsch RR, Lind P, Slightom J;
PS, Bannigan CM, Ruff V, Sejlitz T, Huff RM;
  New G protein-coupled receptor (nGPCR-x) and its encoding polynucleotide useful for diagnosing and treating e.g. schizophrenia
   100.0%; Score 1853; DB 22; Length 346; 100.0%; Pred. No. 1.2e-199;
   Claim 37; Page 89; 261pp; English.
  (PHAA ) PHARMACIA & UPJOHN CO
  2000US-0186530.
2000US-0186811.
2000US-0188114.
  2000US-0190310.
2000US-0190800.
2000US-0198568.
  2000US-0207094.
   99US-0166071
99US-0166678
  2000US-0184129.
2000US-0185421.
   2000US-0185554
  2000US-0201190
   2000US-0203111
   99US-0173396
  2000WO-US31581
   Wood LS, I
A, Kaytes I
  WPI; 2001-389826/41.
  Similarity
   346 AA;
  N-PSDB; AAH51008
neuroprotective.
  WO200136473-A2.
   02-MAR-2000;
03-MAR-2000;
09-MAR-2000;
   Schellin KA,
                         Homo sapiens.
  16-NOV-2000;
  25-MAY-2000;
   28-FEB-2000;
28-FEB-2000;
   21-MAR-2000;
   22-FEB-2000;
  17-MAR-2000;
   20-APR-2000;
   02-MAY-2000;
08-MAY-2000;
   19-NOV-1999
  28-DEC-1999
   Best Local Sim
Matches 346;
  25-MAY-2001
  Vogel1 G,
  Sequence
   Query Match
```

```
Human; GCPR; G-coupled protein-receptor; cardiant; antiarteriosclerotic; anabolic; cytostatic; antiviral; gene therapy; cardiomyopathy; obesity; anotexia; diabetes; osteoporosis; Crohn's disease; multiple sclerosis; asthma; Alzheimer's disease; parkinson's disease; Huntington's disease;
  New human G-protein coupled receptor X, GPCRX, polypeptide useful in
  Spaderna SK;
L1 L;
  Wolenc AR,
Spytek KA,
   infection; human immunodeficiency virus; HIV.
  Vernet CAM, Casman SJ,
Mishnu VS, Tchernev VT,
  2000US-195067P.
2000US-195068P.
2000US-195069P.
   2000US-195070P.
2000US-195510P.
2000US-219855P.
2000US-221284P.
   2000US-194614P
2000US-195063P
  2000US-221325P
  30-MAR-2001; 2001WO-US10241
   2000US-239613P
  2001US-263433P
  2001US-263604P
   Gusev VY;
   (CURA-) CURAGEN CORP
   WPI; 2001-639351/73.
   Baumgartner JC,
  N-PSDB; ABA81531
  WO200174904-A2.
  06-APR-2000; 2
06-APR-2000; 2
06-APR-2000; 2
06-APR-2000; 2
  Homo sapiens.
   06-APR-2000;
21-JUL-2000;
  27-JUL-2000;
28-JUL-2000;
   06-APR-2000;
   11-OCT-2000;
   18-JAN-2001;
   06-APR-2000;
   11-AUG-2000;
  23-JAN-2001;
  23-JAN-2001;
30-JAN-2001;
  Majumder K,
Padigaru M,
   05-APR-2000;
   11-OCT-2001.
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Indels

DFLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHP 120

61

1 MYNGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVA 60 

0; Mismatches

Conservative

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The invention relates to nucleic acid sequences (ABA81529-ABA81552) that encode (2-coupled protein-receptor related polypeptides (ABB4452-ABB44543). The isolated polypeptide having a sequence differing by no more than 15 % of anno acid residues from one of 22 amino acid sequences (or mature forms of the sequences), fully defined in the sequences (or mature forms of the sequences), fully defined in the (GPCRX) polypeptides. The polypeptides have potential cardiant, antiarteriosclerotic, anabolic, cytostatic and antiviral activity. The colypeptides can be administered therapeutically, especially using gene therapy and expressing the encoding DNA in vivo, to treat or prevent CFC GPCRX-associated disorders, especially in humans. For example, they can GPCRX-associated disorders, especially in humans. For example, they can cardiant anorexia), diabetes, osteoporosis, crohn's disease, multiple colopsity, anorexia, distances, neurodegenerative disorders, alsease, parkhnson's disorders, Huntington's disease, immune disorders, haematopoietic disorders, developmental diseases, neurological disorders, haematopoietic disorders, developmental diseases, neurological disorders, condetermine the presence of or predisposition to a disease associated control samples. They are useful to identify agents binding polypeptide control samples. They are useful to identify agents binding polypeptide control samples. They are useful to identify agents binding polypeptide control samples or predisposition or activity.
revention of GPCRX associated disorders e.g. or atherosclerosis, and to screen for antagonists and
  (e.g. cellular receptors or downstream effectors) and/or ayents modulating cellular polypeptide expression or activity, useful as antagonists and agonists in disease treatment.
  Claim 1; Page 11; 157pp; English.
   agonists useful therapeutically
     treatment or prevention
```

Gaps ö Length 346; Indels 99.2%; Score 1839; DB 22; 99.4%; Pred. No. 4.7e-198; 0; Mismatches Best Local Similarity 99.4 Matches 344; Conservative 346 AA; Sequence Query Match

61 DFLLMICLPFRTDXYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAAGRYFKVVHP 120 HHAVNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIM 180 DFLLMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHP 120 1 MYNGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVA 60 61 121 g ò a ò g ò 셤 ò

LYFLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKPK 300 g ò ð

AAG80934 standard; Protein; 296 AA. AAG80934; RESULT 6

(first entry) 28-AUG-2001

Human nGPCR11 #1. DX DX PX

signal transduction; schizophrenia; thyroid disorder; renal failure; rheumatoid arthritis; CNS disorder; infection; metabolic disease; cardiovascular disease; proliferative disorder; hormonal disorder; neurological disorder; neuronal disorder; Alzhelmer's disease; cancer; attention defibit thyperactivity disorder/attention defibit disorder; Parkinson's disease; migraine; senile dementia; inflammatory disease; rheumatoid arthritis; autolmmune disorder; respiratory ailment; protein-coupled receptor; nGPCR; seven transmembrane receptor; neuroprotective

Homo sapiens.

WO200136473-A2.

25-MAY-2001

2000US-0185554 2000US-0186530 2000US-0201190. 99US-0166071 99US-0166678 2000US-0190310 2000US-0190800 2000US-0198568 99US-0173396 2000WO-US31581 2000US-0184129 2000US-0185421 2000US-0186811 2000US-0188114 28-FEB-2000; 02-MAR-2000; 03-MAR-2000; 09-MAR-2000; 16-NOV-2000; 17-MAR-2000; 21-MAR-2000; 02-MAY-2000; 08-MAY-2000; 20-APR-2000; 22-FEB-2000; 28-FEB-2000; 17-NOV-1999; 19-NOV-1999;

(PHAA ) PHARMACIA & UPJOHN CO

2000US-0207094

25-MAY-2000;

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Hiebsch RR, Lind P, Slightom J; Bannigan CM, ĽĄ Parodi I PS, Bar Schellin KA, Kaytes ĽŠ, Wood Vogel1 G,

WPI; 2001-389826/41. N-PSDB; AAH50974 New G protein-coupled receptor (nGPCR-x) and its encoding polynucleotide useful for diagnosing and treating e.g. schizophrenia

Claim 37; Pages 77-78; 261pp; English.

treating neurological disorders, including schizophrenia, ADHD/ADD (attention deficit-hyperactivity disorder/attention deficit disorder), and neuronal disorders such as Alzheimer's disease, Parkinson's disease, migraine and senile dementia. Additional disorders include inflammatory conditions (e.g. Crohn's disease), rheumatoid arthiritis, autoimmune disorders, cancers, respiratory ailments such as asthma, and inflammatory diseases e.g. inflammatory bowel disease. The present invention relates to novel G protein-coupled receptors (nGPCRx; where x is 1, 3, 4, 5, 9, 11, 12, 14-18, 20, 21, 22, 24, 27, 28, 31-38, 40, 41, 53-60) and their coding sequences. The present sequence is one such G protein-coupled receptor. GPCRs are also known as seven transmembrane receptors and function in signal transduction. The nGPCRx coding sequences are useful for screening a human to diagnose a discoperation nGPCRx are useful for screening a human to diagnose a chizophrenia. nGPCRx are useful for identifying compounds useful for treating schizophrenia. Detection of nGPCRx in a sample is useful as a diagnostic tool for diseases or disorders e.g. thyroid disorders, renal failure, rheumatoid arthritis, CNS disorders, infections such as HIV-1, metabolic and cardiovascular diseases, proliferative disorders and hormonal disorders. Modulators of nGPCRx activity have the utility for

296 AA; Sequence

Query Match

Length 296; 84.7%; Score 1570; DB 22;

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  (7TM receptor) family, designated the HM74A receptor. The proteins, agonists, antagonists and polynucleotides can be used for treating disorders associated with increased or reduced expression or activity of HM74A, e.g. bacterial, fungal, protozoan and viral infections, particularly infections caused by HTV-1 or HTV-2, pain, cancers, diabetes, obesity, anorexia, bulimia, asthma, Parkinson's disease, acute heart failure, hypotension, hypertension, urinary retention, osteoporosis, angina pectoris, myocardial infartion, stroke, ulcers, asthma, allergies, benign prostatic hypertrophy, migraine, vomiting, psychotic and neurological disorders, including anxlety, schizophrenia,
  HM74A receptor; G-protein coupled receptor; infection; pain; cancer; diabetes; obesity; neurological disorder; heart failure; hypertension;
   WAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNTISTRVAAGIVCTLW 140
   260
          Gaps
                             LLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMICLPFRTDYYLRRH 80
                                       New isolated G-protein coupled receptor, HM74A - used to develop products for treating e.g. infections, pain, cancers, diabetes, obesity, neurological disorders, heart failure, hypertension, asthma
   present sequence is a member of the G-protein coupled receptor
  ALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIMFQLEFFMPLGIILFCSFKIV
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  Mooney
         Indels
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6.8e-168;
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  Guerrera SF,
          Mismatches
  G-protein coupled receptor HM74A protein.
Pred. No.
   Claim 1; Page 31-32; 40pp; English.
  ¥.
       ;
  AAW94654 standard; Protein; 363
   (SMIK ) SMITHKLINE BEECHAM CORP
   Bergsma DJ, Elshourbagy NA,
100.08;
  98WO-US12386.
  97US-0049480.
   (first entry)
         Conservative
  WPI; 1999-095273/08.
Similarity
   N-PSDB; AAX16671.
   asthma; allergy
  Homo sapiens
   WO9856820-A1
  12-JUN-1997;
  12-JUN-1998;
   allergies
  29-APR-1999
   17-DEC-1998.
   AAW94654;
 Local
   81
   181
   241
                             21
  141
  201
   261
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   AAW94654
   RESULT
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245 WIVPSSA---CD--PSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKP 299
   MICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAV 124
  77 IICLPFLMDNYVRRWDWKFGDIPCRLMLFMLAMNRQGSIIFLTVVAVDRYFRVVHPHHAL 136
   NTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIMFQLE 184
  Gaps
   64
  for
   5 SCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLL
   FFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSARLYFL
manic depression, depression, delirium, dementia, and severe me retardation, and dyskinesias such as Huntington's disease or Gilles de la Tourett's syndrome. The products can also be used detection, diagnosis and drug screening.
  7;
  Length 363;
  Indels
  Human; G-protein coupled receptor; GPCR; hRUP25; agonist;
  300 KOPGHSKTORPEEMPISNLGRRSCISVANSFOSOSDGOWDP 340
   KMTGEPDNNRSTSVELTGDPNKT-RGAPEALMANSGEPWSP 355
  20;
  47.7%; Score 883.5; DB 20;
52.8%; Pred. No. 1.5e-90;
tive 47; Mismatches 107;
   Human G-protein coupled receptor, hRUP25.
  Ş
  AAU04379 standard; Protein; 363
  2000US-0196078.
2000US-0200419.
2000US-0203630.
2000US-0210741.
2000US-0210982.
  990S-0166088.
990S-0166099.
990S-0166369.
990S-0171900.
990S-0171901.
   inverse agonist; lung cancer
  14-MAR-2000; 2000US-0189259.
10-APR-2000; 2000US-0195898.
10-APR-2000; 2000US-0195899.
10-APR-2000; 2000US-0196078.
   2000US-0181749
2000US-0189258
   16-NOV-2000; 2000WO-US31509
  (first entry)
   Local Similarity 52.8
hes 180; Conservative
   363 AA;
   WO200136471-A2
   17-NOV-1999;
23-DEC-1999;
23-DEC-1999;
23-DEC-1999;
   11-FEB-2000;
  Homo sapiens
  14-MAR-2000;
   28-APR-2000;
   12-MAY-2000;
  12-JUN-2000;
  23-OCT-2001
  25-MAY-2001.
  17-NOV-1999
   17-NOV-1999
   AAU04379;
   Sequence
  Query Match
   Best Loca
Matches
   316
   65
   125
   185
   RESULT 8
```

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245 WTVPSSA---CD--PSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKP 299
  20-APR-2000
   Matches 178;
                                 Synthetic
  Sequence
   agents
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   4;
   The sequence represents a human G-protein coupled receptor (GPCR), hRUP55. The endogenous and non-endogenous, constitutively activated versions of human G-protein coupled receptors (GPCR), are useful for direct identification of candidate compounds as receptor agonists, inverse agonists or partial agonists having applicability as therapeutic agents for treating diseases related to GPCR, e.g. lung cancer. Non-endogenous version of human GPCRs are also utilized in research settlings and in vitro and in vivo system, incorporating GPCRs can be utilised to elucidate and understand the roles those receptors play in the human condition, both normal and diseased.
   Endogenous and non-endogenous versions of human G-protein coupled receptors for direct identification of candidate compounds as agonists, inverse agonists or partial agonists for use as therapeutic agents -
  65 MICLPFRIDYYLRRHWAFGDIPCRVGLFILAMNRAGSIVFLTVVAADRYFKVVHPHHAV 124
   125 NTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIMFQLE 184
   Gaps
   SCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLL 64
  FFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSARLYFL
   245 WIVPSSA---CD--PSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKP
   7;
  Length 363;
  G protein-coupled receptor; GPCR; constitutively active; intracellular loop 3; transmembrane domain 6; drug screening;
  47.7%; Score 883.5; DB 22; Length 52.8%; Pred. No. 1.5e-90; ive 47; Mismatches 107; Indels
  Human mutant G protein-coupled receptor HM74 (1230K).
  300 KQPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDP 340
   316 KMTGEPDNNRSTSVELTGDPNKT-RGAPEALMANSGEPWSP 355
  Claim 69; Page 121-122; 160pp; English.
  AAY90672 standard; Protein; 387 AA
   Lowitz KP;
         2000US-0235418.
2000US-0235779.
2000US-0242332.
2000US-0242343.
  (first entry)
   Best Local Similarity 52.8
Matches 180; Conservative
  (AREN-) ARENA PHARM INC
   WPI; 2001-355616/37
   Dang HT,
   363 AA;
  N-PSDB; AAS07952.
21-AUG-2000;
  21-AUG-2000
          26-SEP-2000;
                     26-SEP-2000;
                               20-OCT-2000;
  20-OCT-2000;
   Sequence
   AAY90672;
   Query Match
   Chen R,
   S
  185
   RESULT 9
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The invention relates to constitutively active, non-endogenous versions of endogenous human orphan G protein-coupled receptors (GPCRs, AAY90643-AAY90677 and AAY90683-Y90687), and to DNA encoding them (AAA30709-A30743-AAY90677 and AAA30709-The mutant proteins of the invention contain a mutation in a portion of the protein comprising intracellular loop 3 (IC3) and transmembrane domain 6 (TM6). A non-endogenous amino acid, X, is substituted for an endogenous residue in IC3 at a position 16 amino cids N-terminal of an endogenous proline in TM6 to form a sequence X-(AA)15-Pro. The endogenous amino acid is selected from Lys, His, Arg or AA,15-Pro. The endogenous amino acid is selected by His, Arg or preferably Alas position is Lys, this residue is replaced by His, Arg or preferably Alas position is Lys, this residue is replaced by His, Arg or preferably Alas constitution acid and the Promay be endogenous ron-endogenous, or a mixture of endogenous and con-endogenous residues. The constitutively active GPCRs are useful for identifying antagonists, and partial agonists for use as pharmaceutical agents. The mutant proteins are also useful in research is setting diseases and disorders associated with that receptor. Because the novel mutant GPCRs are constitutively active, they can be used directly for screening of compounds without the need for endogenous continued the acceptor in autant and any active, they can be used directly for screening of compounds without the need for endogenous continued the acceptor and AAY90603-Y90687 the mutant the acceptor and AAY90677 and AAY90687 the mutant
  The invention relates to constitutively active, non-endogenous versions
   65 MICLPFRTDYYLRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAV 124
  125 NTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIMFQLE 184
  Non-endogenous constitutively activated human G protein-coupled receptors, useful for identifying agonists for use as pharmaceutical
  Gaps
  5 SCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLL
  185 FFMPLGIILECSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSARLYFL
   7;
  Length 387;
  47.6%; Score 881.5; DB 21; Length
52.2%; Pred. No. 2.8e-90;
.ive 49; Mismatches 107; Indels
   Example 2; Page 286-287; 341pp; English.
agonist; antagonist; mutant; mutein.
   Liaw CW;
  human GPCRs of the invention.
   98US-0170496
  Conservative
  Behan DP, Chalmers DT,
  (AREN-) ARENA PHARM INC
  Query Match
Best Local Similarity
  WPI; 2000-329165/28
  387 AA;
  N-PSDB; AAA30738
   WO200022129-A1
  Homo sapiens.
   13-OCT-1998;
   12-OCT-1999;
```

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64

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256

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```
Human; G protein-coupled receptor; GPCR; CON103 protein; schizophrenia; neuroleptic; nootropic; neuroprotective; bipolar disease; psychotropic; neurological disorder; psychlatric disease; neurosis; anxiety; neuritis; attention deficit hyperactivity disorder; neurasthenia; senile dementia; affective disorder; neuropathy; Alzheimer's disease; Parkinson's disease, depression; migraine; genetic screening; chromosome 2.
  245 WIVPSSA---CD--PSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKP 299
   MICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAV 124
   125 NTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIMFQLE 184
   185 FFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSARLYFL
   SCCRIEGDIISOVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLL
  NKISNWTAAIISCLLWGITVGLTVHLLKKKLLIQNGPANVCISFSICHTFRWHEAMFLLE
49; Mismatches 107; Indels
   300 KQPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDP 340
  316 KMTGEPDNNRSTSVELTGDPNKT-RGAPEALMANSGEPWSP 355
  /label = Transmembrane_domain_(4TM)
   /label = Transmembrane_domain_(5TM)
  'label = Transmembrane_domain_(1TM)
   Transmembrane_domain_(2TM)
   Transmembrane_domain_(3TM)
   Human CON103 G protein-coupled receptor protein.
  /label= Intracellular_domain
/note= "First IC loop"
  /label = Intracellular_domain
/note = "Second IC loop"
  /label- Extracellular_domain
/note- "Second EC loop"
  /label- Intracellular_domain
/note- "Third IC loop"
  /label- Extracellular_domain
  /note= "First EC loop"
  Location/Qualifiers
   AAE02493 standard; Protein; 384 AA.
  (first entry)
  Conservative
  /note= "T
258..283
   . 133
  149
   .166
   . 215
  240
  .188
   89.,108
  /label=
   label-
  Homo sapiens
   10-AUG-2001
Matches 178;
  AAE02493;
   Domain
   Domain
  Domain
  Domain
  Domain
   Domain
   Domain
   Domain
   Domain
  Domain
  Domain
  137
  RESULT 11
  Key
   AAE02493
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   AAY30673-AAY30683-Y90697), and to DNA encoding them (AAA30709-A30743)
AAY30677-AA30779). The mutant proteins of the invention contain a mutation in a portion of the protein comprising intracellular loop 3
(IC3) and transmembrane domain 6 (TM6). A non-endogenous amino acid, X, is substituted for an endogenous residue in IC3 at a position 16 amino acids N-terminal of an endogenous proline in TM6 to form a sequence X-(AA)15-Pro. The endogenous amino acid is selected from Lys, His, Arg or AA)15-Pro. The endogenous amino acid is selected from Lys, His, Arg position is Lys, this residue is replaced by His, Arg or preferably Ala. The 15 amino acid stretch between the substituted amino acid and the Promay be endogenous. In on-endogenous, non-endogenous, on a mixture of endogenous and non-endogenous residues. The constitutively active GPCRs are useful for identifying antagonists, agonists and partial agonists for use as planmaceutical agents. The mutant proteins are also useful for identifying antagonists for a particular GPCR are useful for diseased conditions. Antagonists for a particular GPCR are useful for treating diseases and disorders associated with that receptor. Because the novel mutant GPCRs are constitutively active, they can be used directly for screening of compounds without the need for endogenous consisting the receptor active, they can be used consistent sequence represents a human wild-type GPCR referred to the and second the active of the and active active active and active a
   The invention relates to constitutively active, non-endogenous versions
  Non-endogenous constitutively activated human G protein-coupled receptors, useful for identifying agonists for use as pharmaceutical
   Score 880.5; DB 21; Length 387;
Pred. No. 3.6e-90;
  G protein-coupled receptor; GPCR; constitutively active; intracellular loop 3; transmembrane domain 6; drug screening;
   300 KQPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDP 340
  316 KMTGEPDNNRSTSVELTGDPNKT-RGAPEALMANSGEPWSP 355
  exemplification of the invention.
  Example 1; Page 185-187; 341pp; English.
  Human G protein-coupled receptor HM74.
   AAY90637 standard; Protein; 387 AA
   Liaw CW;
  47.5%;
   99WO-US23938
  98US-0170496.
  (first entry)
  (AREN-) ARENA PHARM INC.
   Behan DP, Chalmers DT,
  WPI; 2000-329165/28.
N-PSDB; AAA30658.
  agonist; antagonist.
  Query Match
Best Local Similarity
   387 AA;
  WO200022129-A1.
   Homo sapiens
   12-0CT-1999;
  13-OCT-1998;
  21-AUG-2000
  20-APR-2000
  AAY90637;
  Sequence
  in an
  agents
```

216 ALYLLEFFLPLALILFAIVSIGLTIRNR-GLGGQAGPQRAMRVLAMVVAVYTICFLPSII 274

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7;
  dementia. The invention also provides genetic screening procedures that entail analysing a person's genome with respect to GPCR. The vectors are useful for the recombinant production of the GPCR's. The present sequence is human CON103 G protein-coupled receptor (GPCR) protein.
  The invention relates to human G protein-coupled receptor (GPCR) and their corresponding DNA molecules. GPCR is also referred as seven transmembrane receptor. G protein-coupled receptor protein is useful for treating neurological disorder, particularly schizophrenia. GPCR protein is also useful for identifying compounds useful for treating schizophrenia. These compounds are also useful for treating other neurological and psychiatric diseases, e.g. depression, anxiety, bipolar disease, affective disorders, attention deficit hyperactivity disorder, attention deficit disorder, parkinson's disease, migraine and senile neurosis, Alzheimer's disease, Parkinson's disease, migraine and senile
  Seven transmembrane receptor polypeptides and polynucleotides, useful for treating neurological or psychiatric disorders, e.g. schizophrenia, as well as for identifying compounds useful for treating schizophrenia
  LSRASVGAAARVAGGLWVGI-----LLLNGHLLLSTFSGPSCLSYRVGTKPSASLRWHQ 215
  237
  28.5%; Score 529; DB 22; Length 384;
39.2%; Pred. No. 1.2e-50;
.1ve 48; Mismatches 108; Indels 22; Gaps
   64 LMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHA 123
  124 VNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQE-TAVSCESFIM----ESANGWHD 178
  4 GSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFL 63
  179 IMFQLEFFMPLGIILFCSFKIVWSLRRQQLARQARMKKATRFIMVVAIVFITCYLPSV-
'label = Transmembrane_domain_(6TM)
  301..320
/label- Transmembrane_domain_(7TM)
                     284..300
/label- Extracellular_domain
/note- "Third EC loop"
  Claim 1; Page 7-9; 215pp; English.
  Merchant K;
   (PHAA ) PHARMACIA & UPJOHN CO
   99US-0427859.
99US-0428020.
99US-0428114.
99US-0429517.
99US-0429555.
   12-JAN-2000; 2000US-0481794.
   99US-0427653
  99US-0429695
   99US-0454399
  2000WO-US29601
  Query Match
Best Local Similarity 39.29
Matches 115; Conservative
  Wood LS,
   WPI; 2001-328653/34.
   384 AA;
   N-PSDB; AAD06502
   WO200131014-A2
   27-OCT-2000;
  27-OCT-1999;
28-OCT-1999;
28-OCT-1999;
28-OCT-1999;
  28-OCT-1999;
  03-MAY-2001
  27-OCT-1999
   27-OCT-1999
   )3-DEC-1999
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  Seguence
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Domain
  Domain
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This is the amino acid sequence of a novel human G protein coupled receptor, designated HEOAD54, as deduced from a cDNA clone (see AAX06947) isolated from an eosinophil library. A method is claimed for diagnosing susceptibility to disease resulting from mutation of the HEOAD54 gene or imbalance in HEOAD54 polypeptide expression levels. HEOAD54 apointsis/antagonists can be used to activate/inhibit used to prevent expression, while administration of HEOAD54 is used to prevent expression, while administration of HEOAD54 is used to treat conditions associated with a lack of HEOAD54 polypeptide expression. HEOAD54 polypeptides can be administered directly or as a vaccine to inoculate against disease. Diseases diagnosed, prevented and treated include bacterial, immalist, protozoan and concerts, and infections, particularly HIV-1 or HIV-2 infections, pain, concerts, and expression.
  HEOAD54; 7-transmembrane receptor; G protein coupled receptor; signal transduction; human; infection; HIV-1; HIV-2; pain; cancer; anorexia; bulimia; asthma; Parkinson's disease; hypotension; hypertension; acute heart failure; urinary retention; osteoporosis; angina pectoris; myocardial infarction; ulcer; allergy; benign prostatic hypertrophy; anxiety; schlzophrania; delirium; manic demersion; demerlia, severe mental reterdation; dyskinesia; Huntington's disease; Gilles de la Tourette's syndrome; diagnosis;
   New G-protein coupled receptor (HEOAD54) polypeptide and polynucleotide - useful as diagnostic reagents, and for prevention and treatment of HIV infections and cancer
  heart failure, hypotension, hypertension, urinary retention, osteoporosis, angina pectoris, myocardial infarction, ulcer, allergy, benign prostatic hypertrophy, and psychotic and neurological disorders including anxiety, schizophrenia, manic depression, delirium, dementia, severe mental retardation and dyskinesias, such as Huntington's disease or Gilles de la
238 --SARLYFLWTVPSSA---CDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSF
                Sathe GM;
   Human 7-transmembrane receptor HEOAD54.
  Bergsma DJ, Halsey WS, Mooney JL,
  Claim 11; Page 20-21; 25pp; English.
  Š
  AAW88460 standard; Protein; 423
   (SMIK ) SMITHKLINE BEECHAM CORP.
   97US-0955713.
97US-0060124.
  98EP-0304192.
  .0-MAY-1999 (first entry)
   WPI; 1999-083568/08.
   therapy; vaccine.
  N-PSDB; AAX06947
   Homo sapiens
  27 - MAY - 1998;
   33-OCT-1997;
  18-JUN-1997;
  EP892051-A2.
   20-JAN-1999
   AAW88460;
   RESULT 12
   AAW88460
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Tourette's syndrome.

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Gaps

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   LMICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHA 123
  124 VNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQE-TAVSCESFIM----ESANGWHD 178
  179 IMFQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSV- 237
   GSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFL 63
   --SARLYFLWTVPSSA---CDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSF 285
     ; Pred. No. 1.4e-50;
48; Mismatches 108; Indels
  coupled receptor; GPCR; hRUP11; agonist;
  Human G-protein coupled receptor, hRUP11.
  AAU04365 standard; Protein; 423 AA
   28-APR-2000; 2000US-0200419.
12-MAY-2000; 2000US-0203630.
12-UNN-2000; 2000US-0210741.
12-UNN-2000; 2000US-0210982.
21-AUG-2000; 2000US-0235418.
   99US-0171902.
2000US-0181749.
2000US-0189258.
2000US-0189259.
   Chen R, Dang HT, Lowitz KP;
39.28;
  Human; G-protein coupled rec
inverse agonist; lung cancer
  16-NOV-2000; 2000WO-US31509
  2000US-0195898
   2000US-0196078
  2000US-0235779
2000US-0242332
  2000US-0195899
   2000US-0242343
  (first entry)
  Matches 115; Conservative
   WPI; 2001-355616/37
N-PSDB; AAS07938.
     Best Local Similarity
   WO200136471-A2.
  23-DEC-1999;
11-FEB-2000;
14-MAR-2000;
   10-APR-2000;
10-APR-2000;
   Homo sapiens
   14-MAR-2000;
  10-APR-2000;
   23-OCT-2001
  23-DEC-1999;
23-DEC-1999;
  25-MAY-2001
   AAU04365;
  RESULT 14
AAU04365
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  7;
   The present invention provides the protein, cDNA and genomic DNA sequences of human G-protein coupled receptor opioid-type receptor 1 (OTR1). The protein is involved in neurotransmission, and the sequences can be used in the treatment of OTR1 related diseases. The present sequence is the OTR1 protein.
  64 LMICLPFRIDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHA 123
  124, VNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQE-TAVSCESFIM----ESANGWHD 178
   179 IMFQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSV- 237
  :: ||||;|| :||| | ::|| | | ::|| | ::|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| :|| :|| | :|| | :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
   Gaps
  4 GSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKFWYPSTVYLFNLAVADFL 63
   OTR1;
  New opioid-type receptor-1 gene, OTR1, useful for diagnosis and treatment of OTR1-related diseases
  22;
  --SARLYFLWTVPSSA---CDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSF 285
   Length 423;
  28.5%; Score 529; DB 22; Length 423;
  Human; G-protein coupled receptor; opioid-type receptor 1;
neurotransmission.
  Indels
   Score 529; DB 20; Pred. No. 1.4e-50; Hismatches 108;
  AAG78785 standard; Protein; 423 AA.
   48;
  Disclosure; Page 5; 6pp; German.
  Human opioid-type receptor 1.
   28.5%;
ilarity 39.2%;
Conservative 4
   03-MAY-2000; 2000DE-1021475.
  03-MAY-2000; 2000DE-1021475
  N-PSDB; AAI71608, AAI71609
  10-JAN-2002 (first entry)
   Bruess M, Boenisch H;
   WPI; 2001-657613/76.
  (BRUE/) BRUESS M.
(BOEN/) BOENISCH H.
  Similarity
  423 AA;
   423 AA;
   DE10021475-A1
  Homo saptens
  08-NOV-2001.
  Matches 115;
   AAG78785;
   Sequence
  Query Match
  Seguence
   Query Match
   Local
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RESULT 13 AAG78785

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Region
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  Region
 7;
  hRUPII. The endogenous and non-endogenous, constitutively activated versions of human G-protein coupled receptors (GPCR), are useful for direct identification of candidate compounds as receptor agonists, inverse agonists or partial agonists having applicability as therapeutic agents for treating diseases related to GPCR, e.g. lung cancer. Non-endogenous version of human GPCRs are also utilized in research settings and in vitro and in vivo system, incorporating GPCRs can be utilized to elucidate and understand the roles these receptors play in the human condition, both normal and diseased.
                     receptors for direct identification of candidate compounds as agonists, \boldsymbol{\cdot} inverse agonists or partial agonists for use as therapeutic agents \boldsymbol{\cdot}
   Human; HCSRP; cytostatic; antiarthritic; antirheumatic; antiasthmatic; immunosuppressive; antiarterioscalerotic; antibacterial; antiparasitic; neuroprotective; nootropic; anticonvulsant; cancer; leukaemia; melanoma; rheumatoid arthritis; asthma; atherosclerosis; akathesia;
  64 LMICLPFRIDYYLRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHA 123
   124 VNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQE-TAVSCESFIM----ESANGWHD 178
   LSRASVGAAARVAGGLWVGI-----LLLNGHLLLSTFSGPSCLSYRVGTKPSASLRWHQ 254
   179 IMFQLEFFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSV- 237
  sequence represents a human G-protein coupled receptor (GPCR),
         , and non-endogenous versions of human G-protein coupled for direct identification of candidate compounds as agon
  4 GSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFL
   22;
  314 FGMASWVAFWLSACRSLDLCTQLFHG----SLAFTYLNSVLDPVLYCFSSPNF 362
   --SARLYFLWTVPSSA---CDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSF 285
   Length 423;
   28.5%; Score 529; DB 22; Length 4; 39.2%; Pred. No. 1.4e-50; Live 48; Mismatches 108; Indels
  Alzheimer's diseases; multiple sclerosis; epilepsy.
   141..387
/label- Rhodopsin_GPCR_domain
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/label= Transmembrane_domain
   Transmembrane_domain
   ..150
te= "Rhodopsin signature"
  Human cell surface receptor protein #6.
  Claim 13; Page 94-96; 160pp; English
  Location/Qualiflers
  AAY94339 standard; Protein; 455
   (first entry)
   /label= Tr
  Matches 115; Conservative
  /note= "R
159..180
   Similarity
   423 AA;
          Endogenous and
  Homo sapiens
  22-AUG-2000
   Sednence
  Query Match
  AAY94339;
  Local
  Domain
  Jomain
   Domain
   Region
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   RESULT 15
   AAY94339
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The present sequence is a novel human cell surface receptor protein (HCSRP) designated HCSRP-6. The nucleotide sequence was identified in Incyte Clone 2851578 from the CDNA ilbrary BRSTYUTI3, which was made from preast tumour tissue. A number of Incyte Clones were used to assemble the consensus sequence. BLAST analysis showed that the sequence is homologous to rhodopsin-like GPCK/HM14 g219867 isoform 5507827. HCSRP and its antagonist are useful for preventing or treating disorders associated with decreased or increased expression or activity of HCSRP. Such disorders include cancers such as leukaemia and atheroma, immune disorders such as rheumatoid arthritis, asthma and atherosclerosis, bacterial and parasitic infections and neuronal disorders such as akathesia, Alzheimer's disease, multiple sclerosis and expensions to probes to diagnose these conditions. Anti-HCSRP antibodies may be used as antagonists, as a targeting or delivery mechanism for bringing pharmaceutical agents into contact with cells or tissues expressing texapility or immunogenic fragments are useful for drug screening using libraries of compounds.
   New human cell surface receptor protein and polynucleotide useful for diagnosis, prevention and treatment of cancer, immune disorders, infection and neuronal disorders
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   phosphorylation site"
   'note "potential phosphorylation site"
   /note= "potential phosphorylation site"
   'note= "potential phosphorylation site"
   "potential phosphorylation site"
  Yue H, Baughn MR, , Au-Young J;
   'note= "potential glycosylation site"
   'note- "potential glycosylation site"
   phosphorylation
   /note= "potential phosphorylation
   /note= "potential phosphorylation
/note= "Rhodopsin signature"
  "Rhodopsin signature"
   "Rhodopsin signature"
  Tang YT, Corley NC, Guegler KJ, Yu
Hillman JL, Bandman O, Azimzai Y,
   Claim 1; Page 79-80; 97pp; English.
  "Rhodopsin
   'note= "potential
  /note= "potential
207
   /note= "potential
  98US-0206647.
99US-0123404.
   98US-0191280.
   99WO-US26742
   (INCY-) INCYTE PHARM INC.
   .349
   .395
                          204..226
  /note=
  /note=
   /note-
   /note-
  WPI; 2000-376546/32.
N-PSDB; AAA27049.
   WO200028032-A2
   12-NOV-1999;
   08-MAR-1999;
   12-NOV-1998;
   18-MAY-2000
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7;
   124 VNTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQE-TAVSCESFIM----ESANGWHD 178
  179 IMFQLEFFWPLGIILFCSFKIVWSLRRRQQLARQARWKKATRFIMVVAIVFITCYLPSV- 237
  Query Match 28.5%; Score 529; DB 21; Length 455; Best Local Similarity 39.2%; Pred. No. 1.5e-50; Matches 115; Conservative 48; Mismatches 108; Indels 22; Gaps
   4 GSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFL 63
   455 AA;
        Sequence
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The greature intraction tendence to move to procedure tracepouts to GPCRX; where x is 1, 3, 4, 5, 9, 11, 12, 14-18, 20, 21, 22, 24, 27, 28, 31-38, 40, 41, 53-60) and their coding sequences. The present sequence is the coding sequence for one such 6 protein-coupled receptor. Gequence is the coding sequence for one such 6 protein-coupled receptor. Getter also known as seven transmembrane receptors and function in signal transduction. The nGPCRX coding sequences are useful for screening a human to diagnose a disorder affecting the brain or a genetic screening a human to diagnose a disorder affecting the brain or a genetic compounds useful for treating schizophrenia. Detection of nGPCRX in a sample is useful as a diagnostic tool for diseases or disorders e.g. thyroid disorders, renal failure, rheumatoid arthritis, CNS disorders and hormonal disorders. Modulators of diseases, proliferative disorders and hormonal disorders. Modulators of nGPCRX activity have the utility for treating neurological disorders, including schizophrenia, ADHD/ADD (attention deficit-hypersactivity disorder/attention deficit disorder), and neuronal disorders such as Alzheimer's disease, Parkinson's disease, migraine and senile dementia. Alabamatory conditions (e.g. Crohn's allowing the allowing the disorder and the mannance of the answers the property of the answers the allowing the answers the answers the answers the answers the answers and the answers the answers the answers the answers and the answers the answers the answers and answers the answ
   New G protein-coupled receptor (nGPCR-x) and its encoding polynucleotide useful for diagnosing and treating e.g. schizophrenia
  disease), rheumatoid arthritis, autoimmune disorders, cancers, respiratory ailments such as asthma, and inflammatory diseases e.g.
   present invention relates to novel G protein-coupled receptors
   nd P, Slightom J;
Sejlitz T, Huff
  Sequence 1041 BP; 208 A; 294 C; 278 G; 261 T; 0 other;
   Lind
   Ruff V,
   Hiebsch RR,
  disease), rheumatoid arthritis, autoimmune
  Parodi LA, Hiebsch
PS, Bannigan CM,
   Claim 4; Page 89; 261pp; English.
   (PHAA ) PHARMACIA & UPJOHN CO
                       99US-0166071
99US-0166678
  2000US-0190310
  2000US-0201190
   99US-0173396
  2000US-0184129
   2000US-0185421
2000US-0185554
   2000US-0186530
  2000US-0186811
  2000US-0188114
   2000US-0190800
  2000US-0198568
  2000US-0207094
  inflammatory bowel disease
   Kaytes
   Wood LS,
  WPI; 2001-389826/41
   P-PSDB; AAG80968
   03-MAR-2000;
09-MAR-2000;
17-MAR-2000;
   20-APR-2000;
02-MAY-2000;
08-MAY-2000;
                    17-NOV-1999;
19-NOV-1999;
28-DEC-1999;
22-FEB-2000;
  Schellin KA,
  25-MAY-2000;
  28-FEB-2000;
02-MAR-2000;
  21-MAR-2000;
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   Vogeli
  The
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  CTGCTCATTGTGGCCTTTGTGCTGGGCGCACTAGGCCAATGGGGTCGCCCTGTGTGGTTTC 120
  GATITCCICCTTATGATCTGCCTGCCTTTTCGGACAGACTATTACCTCAGACGTAGACAC 240
   Gaps
   09
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  1 ATGTACAACGGGTCGTGCTGCCGCATCGAGGGGGACACCATCTCCCCAGGTGATGCCGCCG
   TGCTTCCACATGAAGACCTGGAAGCCCAGCACTGTTAACCTTTTCAATTTGGCCGTGGCT
 DB 22; Length 1041;
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                        0; Indels
Score 1041; DB 2
Pred. No. 4e-288;
                      Mismatches
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100.0%;
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          Best Local Similarity 100.
Matches 1041; Conservative
  Query Match
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anabolic; cytostatic; antiviral; gene therapy; cardiomyopathy; obesity; anorexia; diabetes; osteoporosis; Crohn's disease; multiple sclerosis; asthma; Alzheimer's disease; Parkinson's disorder; Huntington's disease; infection; human immunodeficiency virus; HIV; ds.
   Human; GCPR; G-coupled protein-receptor; cardiant; antiarteriosclerotic;
   AGGAGTTGCATCAGTGTGGCAAATAGTTTCCAAAGCCAGTCTGATGGGCAATGGGATCCC 1020
           300
                                  360
  360
  420
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   900
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  720
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  780
   780
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  840
   900
  960
                                361 CACCACGCGGTGAACACTATCTCCACCGGGTGGCGGCTGGCATCGTCTGCACCCTGTGG
  GCCCTGGTCATCCTGGGAACAGTGTATCTTTGCTGGAGAACCATCTCTGCGTGCAAGAG
   GCCCTGGTCATCCTGGGAACAGTGTATCTTTTGCTGGAGAACCATCTCTGCGTGCAAGAG
  TGGAGCCTGAGGCGGAGGCAGCTGGCCAGACAGGCTCGGATGAAGAAGGCGACCCGG
  CTCTATTTCCTCTGGACGGTGCCCTCGAGTGCCTGCGATCCCTCTGTCCATGGGGCCCTG
   TCAAGCCCCTCCTTTCCCAAATTCTACAACAAGCTCAAAATCTGCAGTCTGAAACCCAAG
  CACCACGCGGTGAACACTATCTCCACCCGGGTGGCGGCTGGCATCGTCTGCACCCTGTGG
  TTCATCATGGTGGTGGCAATTGTGTTCATCACATGCTACCTGCCCAGCGTGTCTGCTAGA
   CTCTATTTCCTCTGGACGGTGCCCTCGAGTGCCTGCGATCCCTCTGTCCATGGGGCCCTG
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   TICCAGCIGGAGTICTITATGCCCCTCGGCATCATCTTATTTTGCTCCTTCAAGATTGTT
   CACATAACCCTCAGCTTCACCTACATGAACAGCATGCTGGATCCCCTGGTGTATTTTT
  Human GPCRla polynucleotide SEQ ID NO 1.
  CACATTGTTGAGTGGCACTGA 1041
   BP.
   1021 CACATTGTTGAGTGGCACTGA 1041
  ABA81529 standard; DNA; 1050
   (first entry)
  28-JAN-2002
  181
   541
  541
  661
  721
  841
  1021
   421
  421
   601
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  721
   781
  781
  901
  901
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  ABA81529
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  The present sequence is a member of the G-protein coupled receptor (7TM receptor) family, designated the HM74A receptor. The proteins, agonists, antagonists and polynucleotides can be used for treating disorders associated with increased or reduced expression or activity of HM74A, e.g. bacterial, fungal, protozoan and viral infections, particularly infections caused by HIV-1 or HIV-2, pain, cancers, disbetes, obesity, anorexia, bulimia, asthma, Parkinson's disease, acute heart failure, hypotension, hypertension, urinary retention, osteoporosis, angina pectoris, myocardial infarction, stroke, ulcers, asthma, allergies, benign prostatic hypertrophy, migraine, vomiting, psychotic and neurological disorders, including anxiety, schizophrenia,
  HM74A receptor; G-protein coupled receptor; infection; pain; cancer;
diabetes; obesity; neurological disorder; heart failure; hypertension;
  WAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAVNTISTRVAAGIVCTLW 140
  ALVILGIVYLLLENHLCVQETAVSCESFIMESANGWHDIMFQLEFFMPLGIILFCSFKIV 180
   ALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIMFQLEFFMPLGIILFCSFKIV 200
   WSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSARLYFLWTVPSSACDPSVHGAL 260
   240
                              Gaps
   New isolated G-protein coupled receptor, HM74A - used to develop products for treating e.g. infections, pain, cancers, diabetes, obesity, neurological disorders, heart failure, hypertension, asthma
   LLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLLMICLPFRTDYYLRRH 80
  ó
  Mooney
                            Indels
   L1 X,
            Pred. No. 6.8e-168;
Hismatches 0;
   Guerrera SF,
   G-protein coupled receptor HM74A protein.
  Claim 1; Page 31-32; 40pp; English.
  AAW94654 standard; Protein; 363 AA
100.08; Fr
   (SMIK ) SMITHKLINE BEECHAM CORP.
  Bergsma DJ, Elshourbagy NA,
   98WO-US12386
   97US-0049480
   (first entry)
                         Conservative
  WPI; 1999-095273/08.
            Similarity
   N-PSDB; AAX16671.
  asthma; allergy
   Homo sapiens
   WO9856820-A1
  12-JUN-1997;
   12-JUN-1998;
   29-APR-1999
   or allergies
  17-DEC-1998
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   21
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   141
  61
  121
   201
  181
   261
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   AAW94654
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245 WTVPSSA---CD--PSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKP 299
   185 FFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSARLYFL 244
   65 MICLPFRTDYYLRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAV 124
   125 NTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIMFQLE 184
   Gaps
  5 SCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLL 64
                         for
manic depression, depression, delirium, dementia, and severe me retardation, and dyskinesias such as Huntington's disease or Gilles de la Tourett's syndrome. The products can also be used detection, diagnosis and drug screening.
  Length 363;
  47; Mismatches 107; Indels
  receptor; GPCR; hRUP25; agonist;
   300 KOPGHSKTORPEEMPISNLGRRSCISVANSFOSOSOGGWDP 340
  KMTGEPDNNRSTSVELTGDPNKT-RGAPEALMANSGEPWSP 355
   DB 20;
   47.7%; Score 883.5; DB 2
52.8%; Pred. No. 1.5e-90;
   Human G-protein coupled receptor, hRUP25
   Z
  AAU04379 standard; Protein; 363
   coupled rece
lung cancer.
  990S-0166088.
990S-0166099.
990S-0166369.
990S-0171900.
  99US-0171902.
2000US-0181749.
2000US-0189258.
   2000US-0195898
2000US-0195899
   2000WO-US31509
  2000US-0189259
  000US-0196078
   2000US-0200419
  2000US-0203630
   2000US-0210982
  (first entry)
  Matches 180; Conservative
   Similarity
   363 AA;
  G-protein
  inverse agonist;
   WO200136471-A2.
  23-DEC-1999;
11-FEB-2000;
14-MAR-2000;
   Homo sapiens.
   16-NOV-2000;
  10-APR-2000;
  10-APR-2000;
   10-APR-2000;
  14-MAR-2000;
   28-APR-2000;
  12-JUN-2000;
  23-OCT-2001
  25-MAY-2001.
  17-NOV-1999;
17-NOV-1999;
  23-DEC-1999;
  17-NOV-1999
  23-DEC-1999
  Sequence
   AAU04379;
   Query Match
   Local
  Human;
   137
  316
  AAU04379
  RESULT
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AAH51053 standard; DNA; 24 BP.

RESULT 15 AAH51053 (first entry)

28-AUG-2001

AAH51053;

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The present sequence encodes a member of the G-protein coupled receptor (7TM receptor) family, designated the HW74A receptor. The proteins, agonists, antagonists and polynuclectides can be used for treating disorders associated with increased or reduced expression or activity of HM74A, e.g. bacterial, fungal, protozoan and viral infections.

C HM74A, e.g. bacterial, fungal, protozoan and viral infections.

C diabetes, obesity, anorexia, bulimia, astima, Parkinson's disease, acute heart failure, hypotension, hypertension, urinary retention, osteoporosis, angina pectoris, myocardial infarction, stroke, ulcers, asthma, allergies, benign prostatic hypertrophy, migraine, vomiting, psychotic and neurological disorders, including anxiety, schizophrenia, manic depression, depression, delirium, dementia, and severe mental retardation, and dyskinesias such as Huntington's disease or discretices.
  HM74A receptor; G-protein coupled receptor; infection; pain; cancer; diabetes; obesity; neurological disorder; heart failure; hypertension; asthma; allergy; ss.
  New isolated G-protein coupled receptor, HM74A - used to develop products for treating e.g. infections, pain, cancers, diabetes, obesity, neurological disorders, heart failure, hypertension, asthma
   Li X, Mooney JL;
  Length 1361;
  Sequence 1361 BP; 291 A; 390 C; 342 G; 338 T; 0 other;
   Score 32; DB 20; I
Pred. No. 8.9e-06;
  G-protein coupled receptor HM74A encoding cDNA.
  3.1%; Sco...
100.0%; Pred. No. c...
... 0; Mismatches
   Bergsma DJ, Elshourbagy NA, Guerrera SF,
  /product "HM74A receptor"
               790 CTCAGCTTCACCTACATGAACAGCATGCTGGA 821
   detection, diagnosis and drug screening
   Location/Qualifiers
61..1152
   Claim 2; Page 30-31; 40pp; English.
   AAX16671 standard; cDNA; 1361 BP
   (SMIK ) SMITHKLINE BEECHAM CORP.
  970S-0049480
   98WO-US12386
   29-APR-1999 (first entry)
   Query Match
Best Local Similarity 100.
Matches 32; Conservative
  /*tag=
  WPI; 1999-095273/08.
P-PSDB; AAW94654.
  12-JUN-1997;
   allergies
   WO9856820-A1
   Homo saptens
   12-JUN-1998;
  17-DEC-1998.
   AAX16671;
   AAX1667
   셤
   ð
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The present invention relates to novel G protein-coupled receptors

(nGPCRx; where x is 1, 3, 4, 5, 9, 11, 12, 14-18, 20, 21, 22, 24, 27,

(28, 31-38, 40, 41, 53-60) and their codding sequences (see

28, 31-38, 40, 41, 53-60) and their codding sequences (see

AMENGO969-AAMESIOIS and AAMESIOS and AAG80929-AAG80975 and AAG80977). The

present sequence is an oligonucleotide, which was used in the present

invention. GPCRs are also known as seven transmembrane receptors and

threating a human to diagnose a disorder affecting the brain or a

conformation in signal transduction. The nGPCRx according sequences are useful

conformation in signal transduction. The nGPCRx are useful

conformation in signal transduction and isociting the brain or a

genetic predisposition, specifically schizophrenia. nGPCRx are useful

conformation in signal and in a diagnostic tool for diseases or

disorders e.g. thyroid disorders, renal fallure, rheumatoid arthritis,

closurders e.g. thyroid disorders, renal fallure, rheumatoid arthritis,

closurders, infections such as HIV-1, metabolic and cardlowsacular

conformation in disorders and hormonal disorders. Modulators of
  G protein-coupled receptor; nGPCR; seven transmembrane receptor; signal transduction; schizophrenia; thyroid disorder; renal failure; rheumatoid arthritis; CNS disorder; infection; metabolic disease; cardiovascular disease; proliferative disorder; hormonal disorder; neurological disorder; neuronal disorder; Alzheimer's disease; cancer; attention deficit hyperactivity disorder/attention deficit disorder; Parkinson's disease; migraine; senile dementia; inflammatory disease; rheumatoid arthritis; autoimmune disorder; respiratory ailment;
   Parodi LA, Hiebsch RR, Lind P, Slightom J;
PS, Bannigan CM, Ruff V, Sejlitz T, Huff RM;
  New G protein-coupled receptor (nGPCR-x) and its encoding polynucleotide useful for diagnosing and treating e.g. schlzophrenia
  Disclosure; Page 246; 261pp; English
  (PHAA ) PHARMACIA & UPJOHN CO
  99US-0166071.
99US-0166678.
99US-0173396.
2000US-0184129.
2000US-0185421.
  2000US-0203111.
2000US-0207094.
   2000US-0190310
   2000US-0201190
   2000US-0185554
2000US-0186530
  2000US-0190800
   2000US-0198568
  16-NOV-2000; 2000WO-US31581
  2000US-0186811
   2000US-0188114
   Oligonucleotide SEQ ID 133.
  Schellin KA, Kaytes
   WPI; 2001-389826/41.
  neuroprotective; ss.
   Wood LS,
  WO200136473-A2.
  21-MAR-2000;
20-APR-2000;
02-MAY-2000;
   28-FEB-2000;
  02-MAR-2000;
03-MAR-2000;
   25-MAY-2000;
  22-FEB-2000;
   09-MAR-2000;
   17-MAR-2000;
   19-NOV-1999;
   28-DEC-1999;
  08-MAY-2000
   25-MAY-2001
   Vogeli G,
   Synthetic.
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Gaps

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0; Indels

790 CTCAGCTTCACCTACATGAACAGCATGCTGGA 821

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